



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 15966-776CIP

This patent application of

GERLACH, VALERIE L. et al.

Serial No. 09/898,570

Filed: July 3, 2001

For: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
USING THE SAME

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

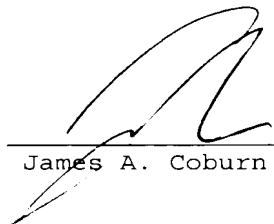
1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/898,570

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Oct. 1, 2001
Date


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SEQUENCE LISTING

<110> GERLACH, VALERIE L.
ELLERMAN, KAREN
MACDOUGALL, JOHN R.
SMITHSON, GLENNDA

<120> NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
METHODS OF USING THE SAME

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| Leu | His | Ile | Glu | Asp | Asn | Asp | Phe | Ala | Met | Arg | Pro | Gly | Phe | Gly | Gly |
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| Ile | Ser | Glu | Thr | Asn | Met | Asp | Phe | Thr | Met | Thr | Phe | Tyr | Leu | Arg | His |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Tyr | Trp | Lys | Asp | Glu | Arg | Leu | Ser | Phe | Pro | Ser | Thr | Ala | Asn | Lys | Ser |
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| Leu | Tyr | Leu | Leu | Tyr | Cys | Gln | Arg | Ser | Phe | Phe | Ser | Pro | Ser | Ser | Ile |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Pro | Ser | Ser | Pro | Asp | Ile | His | Ala | Pro | Gly | Thr | Ser | Lys | Ser | Ser |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Ser | Asp | Ser | Leu | Val | Cys | Ile | Ser | Glu | Lys | Asn | Leu | Pro | Gly | His |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ser | Lys | Asn | Thr | Pro | Leu | Ala | Met | Ser | Asp | Val | Ala | Tyr | Asn | Glu | Asp |
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| Glu | His | Met | Ser | Leu | Ser | Gln | Phe | Phe | Ile | Glu | Asp | Phe | Ser | Ala | Ser |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ser | Gly | Leu | Ala | Phe | Tyr | Ser | Ser | Thr | Gly | Thr | Ala | Phe | Tyr | Met | Gly |
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| Trp | Val | Ile | Thr | Arg | Ala | Met | Asp | Lys | Lys | Met | Glu | Met | Gly | Ile | Thr |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Thr | Val | Leu | Thr | Met | Ser | Thr | Ile | Ile | Thr | Ala | Val | Ser | Ala | Ser | Met |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Pro | Gln | Val | Ser | Tyr | Leu | Lys | Ala | Val | Asp | Val | Tyr | Leu | Trp | Val | Ser |
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Leu Thr Thr Val Glu Glu Arg Lys Gln Phe Lys Lys Ser Phe Ser Lys
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Gly Cys Tyr His Asp Ser Glu Ile Asp Met Asp Gln Thr Ser Leu Ser
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Leu Asn Ser Glu Asp Phe Met Arg Arg Lys Ser Ile Cys Ser Pro Ser
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Thr Asp Ser Ser Arg Ile Lys Arg Arg Lys Ser Leu Gly Gly His Val
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Gly Arg Ile Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg
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 35 40 45
 Asp Ser Thr Lys Ala Arg Pro Gln Lys Tyr Glu Gln Leu Leu His Ile
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 Glu Asp Asn Asp Phe Ala Met Arg Pro Gly Phe Gly Gly Ser Pro Val
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 Pro Val Gly Ile Asp Val His Val Glu Ser Ile Asp Ser Ile Ser Glu
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 Asp Glu Arg Leu Ser Phe Pro Ser Thr Ala Asn Lys Ser Met Thr Phe
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 Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
 180 185 190
 Gln Asn Cys Ser Leu Glu Leu Glu Ser Ala Tyr Asn Glu Asp Asp Leu
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 290 295 300
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 Val Ser Tyr Leu Lys Ala Val Asp Val Tyr Leu Trp Val Ser Ser Leu
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Arg Cys Ser Ser Ser Met Lys Gln Thr Cys Lys Gln Glu Thr Arg Met
    35              40              45

Lys Lys Asp Asp Ser Thr Lys Ala Arg Pro Gln Lys Tyr Glu Gln Leu
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Leu His Ile Glu Asp Asn Asp Phe Ala Met Arg Pro Gly Phe Gly Gly
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Ser Pro Val Pro Val Gly Ile Asp Ala His Val Glu Ser Ile Asp Ser
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Ile Ser Glu Thr Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His
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Tyr Trp Lys Asp Glu Arg Leu Ser Phe Pro Ser Thr Ala Asn Lys Ser
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| Phe | Phe | Val | His | Ser | Lys | Arg | Ser | Phe | Ile | His | Asp | Thr | Thr | Met | Glu | 145 | 150 | 155 |
| Asn | Ile | Met | Leu | Arg | Val | His | Pro | Asp | Gly | Asn | Val | Leu | Leu | Ser | Leu | 165 | 170 | 175 |
| Arg | Ile | Thr | Val | Ser | Ala | Met | Cys | Phe | Met | Asp | Phe | Ser | Arg | Phe | Pro | 180 | 185 | 190 |
| Leu | Asp | Asp | Thr | Gln | Asn | Cys | Ser | Leu | Glu | Leu | Glu | Ser | Cys | Ala | Tyr | 195 | 200 | 205 |
| Asn | Glu | Asp | Asp | Leu | Met | Leu | Tyr | Trp | Lys | His | Gly | Asn | Lys | Ser | Leu | 210 | 215 | 220 |
| Asn | Thr | Glu | Glu | His | Met | Ser | Leu | Ser | Gln | Phe | Phe | Ile | Glu | Asp | Phe | 225 | 230 | 235 |
| Ser | Ala | Ser | Ser | Gly | Leu | Ala | Phe | Tyr | Ser | Ser | Thr | Gly | Trp | Tyr | Asn | 245 | 250 | 255 |
| Arg | Leu | Phe | Ile | Asn | Phe | Val | Leu | Arg | Arg | His | Val | Phe | Phe | Phe | Val | 260 | 265 | 270 |
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| Ser | Phe | Trp | Ile | Asp | Arg | Arg | Ala | Val | Pro | Ala | Arg | Val | Ser | Leu | Gly | 290 | 295 | 300 |
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| Ser | Met | Pro | Gln | Val | Ser | Tyr | Leu | Lys | Ala | Val | Asp | Val | Tyr | Leu | Trp | 325 | 330 | 335 |
| Val | Ser | Ser | Leu | Phe | Val | Phe | Leu | Ser | Val | Ile | Glu | Tyr | Ala | Ala | Val | 340 | 345 | 350 |
| Asn | Tyr | Leu | Thr | Thr | Val | Glu | Glu | Arg | Lys | Gln | Phe | Lys | Lys | Thr | Gly | 355 | 360 | 365 |
| Lys | Val | Ser | Arg | Met | Tyr | Asn | Ile | Asp | Ala | Val | Gln | Ala | Met | Ala | Phe | 370 | 375 | 380 |
| Asp | Gly | Cys | Tyr | His | Asp | Ser | Glu | Ile | Asp | Met | Asp | Gln | Thr | Ser | Leu | 385 | 390 | 395 |
| Ser | Leu | Asn | Ser | Glu | Asp | Phe | Met | Arg | Arg | Lys | Ser | Ile | Cys | Ser | Pro | 405 | 410 | 415 |
| Ser | Thr | Asp | Ser | Ser | Arg | Ile | Lys | Arg | Arg | Lys | Ser | Leu | Gly | Gly | His | 420 | 425 | 430 |

Val Gly Arg Ile Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser
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CG54683-03

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| Lys | Lys | Asp | Asp | Ser | Thr | Lys | Ala | Arg | Pro | Gln | Lys | Tyr | Glu | Gln | Leu | | |
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| Ile | Ser | Glu | Thr | Asn | Met | Asp | Phe | Thr | Met | Thr | Phe | Tyr | Leu | Arg | His | | |
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| Tyr | Trp | Lys | Asp | Glu | Arg | Leu | Ser | Phe | Pro | Ser | Thr | Ala | Asn | Lys | Ser | | |
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| Phe | Phe | Val | His | Ser | Lys | Arg | Ser | Phe | Ile | His | Asp | Thr | Thr | Met | Glu | | |
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| Asn | Ile | Met | Leu | Arg | Val | His | Pro | Asp | Gly | Asn | Val | Leu | Leu | Ser | Leu | | |
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| Leu | Thr | Gln | Asn | Cys | Ser | Leu | Glu | Leu | Glu | Ser | Cys | Ala | Tyr | Asn | Glu | | |
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| Trp | Ile | Asp | Arg | Arg | Ala | Val | Pro | Ala | Arg | Val | Ser | Leu | Gly | Ile | Thr | | |
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| Thr | Val | Leu | Thr | Met | Ser | Thr | Ile | Ile | Thr | Ala | Val | Ser | Ala | Ser | Met | | |
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Z97832_B.0.704

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| gccatcaaa | g | tgtttccttg | acagcggtcg | cagaagttct | gacggaagtc | 2220 |
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| acactgctcc | gtctggccgt | ggttaatacgt | tccttgccgg | cagctgacac | acttggtccc | 2640 |
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| gcccactgtg | ttgcggcaaa | tatggtcaca | gccccggttg | tttaagcggc | actcatctat | 3600 |
| atctttgcac | gtcttcctgt | ctggctgcag | catgaagccc | acagggcgag | tgagtgagac | 3660 |
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| atcacacgtg | tgctggcagc | cgccgttacc | atagttgcat | gtcaatttac | agtcctgttg | 3900 |
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| ccggcaaatg | tgggcacagc | cgtggttctt | gttcacgcaa | ttcattcctt | cttctggccg | 4020 |
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| gtaattgcca | gggatgttga | cacagtcatg | cacacaacct | gcattatcct | ctcgctcgca | 4260 |
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```

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<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

Z97832_B.0.707

<400> 12

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```

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Asp Asn Gln His Thr Cys Ile Gln Arg Pro Glu Glu Gly Met Asn Cys
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```

```

Met Asn Lys Asn His Gly Cys Ala His Ile Cys Arg Glu Thr Pro Lys
          35                      40                      45

```

```

Gly Gly Ile Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Thr Lys Asn
 50                      55                      60

```

```

Gln Arg Asp Cys Lys Leu Thr Cys Asn Tyr Gly Asn Gly Gly Cys Gln
 65                      70                      75                      80

```

```

His Thr Cys Asp Asp Thr Glu Gln Gly Pro Arg Cys Gly Cys His Ile
          85                      90                      95

```

```

Lys Phe Val Leu His Thr Asp Gly Lys Thr Cys Ile Gly Glu Arg Arg
          100                      105                      110

```

```

Leu Glu Gln His Ile Pro Thr Gln Ala Val Ser Asn Glu Thr Cys Ala
          115                      120                      125

```

```

Val Asn Asn Gly Gly Cys Asp Ser Lys Cys His Asp Ala Ala Thr Gly
          130                      135                      140

```

```

Val His Cys Thr Cys Pro Val Gly Phe Met Leu Gln Pro Asp Arg Lys
          145                      150                      155                      160

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Thr Cys Lys Asp Ile Asp Glu Cys Arg Leu Asn Asn Gly Gly Cys Asp
          165                      170                      175

```

```

His Ile Cys Arg Asn Thr Val Gly Ser Phe Glu Cys Ser Cys Lys Lys
          180                      185                      190

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Gly Tyr Lys Leu Leu Ile Asn Glu Arg Asn Cys Gln Asp Ile Asp Glu
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 Cys Ser Phe Asp Arg Thr Cys Asp His Ile Cys Val Asn Thr Pro Gly
 210 215 220
 Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly Ile Thr
 225 230 235 240
 His Cys Gly Asp Val Asp Glu Cys Ser Ile Asn Arg Gly Gly Cys Arg
 245 250 255
 Phe Gly Cys Ile Asn Thr Pro Gly Ser Tyr Gln Cys Thr Cys Pro Ala
 260 265 270
 Gly Gln Gly Arg Leu His Trp Asn Gly Lys Asp Cys Thr Glu Pro Leu
 275 280 285
 Lys Cys Gln Gly Ser Pro Gly Ala Ser Lys Ala Met Leu Ser Cys Asn
 290 295 300
 Arg Ser Gly Lys Lys Asp Thr Cys Ala Leu Thr Cys Pro Ser Arg Ala
 305 310 315 320
 Arg Phe Leu Pro Glu Ala Ala Val Leu Ser Ile Lys Gln Arg Ala Ser
 325 330 335
 Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu Arg Asn Lys Gly
 340 345 350
 Lys Thr Glu Glu Ala Gly Arg Thr Thr Gly Pro Gly Gly Ala Pro Cys
 355 360 365
 Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys Asp Ser Ser Arg
 370 375 380
 Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly Lys Glu Val Thr
 385 390 395 400
 Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala Glu Glu Thr Thr
 405 410 415
 Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met Glu Arg Arg Leu
 420 425 430
 Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn Gln Asp Arg Phe
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 Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala His Lys Pro Gly
 450 455 460
 Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser Cys Arg Pro Gly
 465 470 475 480
 Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro Gln Gly Thr Tyr
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Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro Ala Gly Thr Phe
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 Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys Pro Gly Ser Asp
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 Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr Cys Ala Gly Gln
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 Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys Pro Cys Gln Pro
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 Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg Thr Leu Cys Phe
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 Pro Cys Gly Gly Gly Leu Thr Thr Lys His Glu Gly Ala Ile Ser Phe
 580 585 590
 Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly His Tyr Tyr Asn
 595 600 605
 Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly Ser Tyr Gln Pro
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 Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly Asn Thr Ser Thr
 625 630 635 640
 Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys Asn Arg Gln Cys
 645 650 655
 Gly Gly Glu Leu Gly Glu Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr
 660 665 670
 Pro Gly Asn Tyr Pro Ala Gly Val Glu Cys Ile Trp Asn Ile Asn Pro
 675 680 685
 Pro Pro Lys Arg Lys Ile Leu Ile Val Val Pro Glu Ile Phe Leu Pro
 690 695 700
 Ser Glu Asp Glu Cys Gly Asp Val Leu Val Met Arg Lys Asn Ser Ser
 705 710 715 720
 Pro Ser Ser Ile Thr Thr Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro
 725 730 735
 Ile Ala Phe Thr Ala Arg Ser Arg Lys Leu Trp Ile Asn Phe Lys Thr
 740 745 750
 Ser Glu Ala Asn Ser Ala Arg Gly Phe Gln Ile Pro Tyr Val Thr Tyr
 755 760 765
 Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val Arg Asp Gly Arg
 770 775 780
 Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys Asp Lys Lys Leu
 785 790 795 800

Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln Asn Tyr Phe Lys
805 810 815

Tyr Thr Glu Lys His Lys Glu Met Leu Pro Lys Ser Phe Ile Lys Leu
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Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr Lys
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<211> 4550

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
Z97832_B_1

<400> 13

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<211> 974

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
Z97832_B_1

<400> 14

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His Ala Arg Ala Ala Gln Tyr Ser Lys Ala Ala Gln Asp Val Asp Glu
    20                      25                      30

```

```

Cys Val Glu Gly Thr Asp Asn Cys His Ile Asp Ala Ile Cys Gln Asn
    35                      40                      45

```

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Pro | Arg | Ser | Tyr | Lys | Cys | Ile | Cys | Lys | Ser | Gly | Tyr | Thr | Gly | Asp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Gly | Lys | His | Cys | Lys | Asp | Val | Asp | Glu | Cys | Glu | Arg | Glu | Asp | Asn | Ala | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Gly | Cys | Val | His | Asp | Cys | Val | Asn | Ile | Pro | Gly | Asn | Tyr | Arg | Cys | Thr | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Cys | Tyr | Asp | Gly | Phe | His | Leu | Ala | His | Asp | Gly | His | Asn | Cys | Leu | Asp | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Val | Asp | Glu | Cys | Ala | Glu | Gly | Asn | Gly | Gly | Cys | Gln | Gln | Ser | Cys | Val | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Asn | Met | Met | Gly | Ser | Tyr | Glu | Cys | His | Cys | Arg | Glu | Gly | Phe | Phe | Leu | |
| 130 | | | | | | 135 | | | | | 140 | | | | | |
| Ser | Asp | Asn | Gln | His | Thr | Cys | Ile | Gln | Arg | Pro | Glu | Glu | Gly | Met | Asn | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Cys | Met | Asn | Lys | Asn | His | Gly | Cys | Ala | His | Ile | Cys | Arg | Glu | Thr | Pro | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Lys | Gly | Gly | Ile | Ala | Cys | Glu | Cys | Arg | Pro | Gly | Phe | Glu | Leu | Thr | Lys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Asn | Gln | Arg | Asp | Cys | Lys | Leu | Thr | Cys | Asn | Tyr | Gly | Asn | Gly | Gly | Cys | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Gln | His | Thr | Cys | Asp | Asp | Thr | Glu | Gln | Gly | Pro | Arg | Cys | Gly | Cys | His | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Ile | Lys | Phe | Val | Leu | His | Thr | Asp | Gly | Lys | Thr | Cys | Ile | Gly | Glu | Arg | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Arg | Leu | Glu | Gln | His | Ile | Pro | Thr | Gln | Ala | Val | Ser | Asn | Glu | Thr | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ala | Val | Asn | Asn | Gly | Gly | Cys | Asp | Ser | Lys | Cys | His | Asp | Ala | Ala | Thr | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Gly | Val | His | Cys | Thr | Cys | Pro | Val | Gly | Phe | Met | Leu | Gln | Pro | Asp | Arg | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Lys | Thr | Cys | Lys | Asp | Ile | Asp | Glu | Cys | Arg | Leu | Asn | Asn | Gly | Gly | Cys | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Asp | His | Ile | Cys | Arg | Asn | Thr | Val | Gly | Ser | Phe | Glu | Cys | Ser | Cys | Lys | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Lys | Gly | Tyr | Lys | Leu | Leu | Ile | Asn | Glu | Arg | Asn | Cys | Gln | Asp | Ile | Asp | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Glu | Cys | Ser | Phe | Asp | Arg | Thr | Cys | Asp | His | Ile | Cys | Val | Asn | Thr | Pro | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |

Gly Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly Ile
 355 360 365
 Thr His Cys Gly Asp Val Asp Glu Cys Ser Ile Asn Arg Gly Gly Cys
 370 375 380
 Arg Phe Gly Cys Ile Asn Thr Pro Gly Ser Tyr Gln Cys Thr Cys Pro
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 Ala Gly Gln Gly Arg Leu His Trp Asn Gly Lys Asp Cys Thr Glu Pro
 405 410 415
 Leu Lys Cys Gln Gly Ser Pro Gly Ala Ser Lys Ala Met Leu Ser Cys
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 Asn Arg Ser Gly Lys Lys Asp Thr Cys Ala Leu Thr Cys Pro Ser Arg
 435 440 445
 Ala Arg Phe Leu Pro Glu Ala Ala Val Leu Ser Ile Lys Gln Arg Ala
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 Ser Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu Arg Asn Lys
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 Gly Lys Thr Glu Glu Ala Gly Arg Thr Thr Gly Pro Gly Gly Ala Pro
 485 490 495
 Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys Asp Ser Ser
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 Arg Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly Lys Glu Val
 515 520 525
 Thr Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala Glu Glu Thr
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 Thr Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met Glu Arg Arg
 545 550 555 560
 Leu Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn Gln Asp Arg
 565 570 575
 Phe Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala His Lys Pro
 580 585 590
 Gly Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser Cys Arg Pro
 595 600 605
 Gly Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro Gln Gly Thr
 610 615 620
 Tyr Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro Ala Gly Thr
 625 630 635 640
 Phe Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys Pro Gly Ser
 645 650 655

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ala | His | Gly | Pro | Leu | Gly | Ala | Thr | Asn | Val | Thr | Thr | Cys | Ala | Gly | 660 | 665 | 670 | |
| Gln | Cys | Pro | Pro | Gly | Gln | His | Ser | Val | Asp | Gly | Phe | Lys | Pro | Cys | Gln | 675 | 680 | 685 | |
| Pro | Cys | Pro | Arg | Gly | Thr | Tyr | Gln | Pro | Glu | Ala | Gly | Arg | Thr | Leu | Cys | 690 | 695 | 700 | |
| Phe | Pro | Cys | Gly | Gly | Gly | Leu | Thr | Thr | Lys | His | Glu | Gly | Ala | Ile | Ser | 705 | 710 | 715 | 720 |
| Phe | Gln | Asp | Cys | Asp | Thr | Lys | Val | Gln | Cys | Ser | Pro | Gly | His | Tyr | Tyr | 725 | 730 | 735 | |
| Asn | Thr | Ser | Ile | His | Arg | Cys | Ile | Arg | Cys | Ala | Met | Gly | Ser | Tyr | Gln | 740 | 745 | 750 | |
| Pro | Asp | Phe | Arg | Gln | Asn | Phe | Cys | Ser | Arg | Cys | Pro | Gly | Asn | Thr | Ser | 755 | 760 | 765 | |
| Thr | Asp | Phe | Asp | Gly | Ser | Thr | Ser | Val | Ala | Gln | Cys | Lys | Asn | Arg | Gln | 770 | 775 | 780 | |
| Cys | Gly | Gly | Glu | Leu | Gly | Glu | Phe | Thr | Gly | Tyr | Ile | Glu | Ser | Pro | Asn | 785 | 790 | 795 | 800 |
| Tyr | Pro | Gly | Asn | Tyr | Pro | Ala | Gly | Val | Glu | Cys | Ile | Trp | Asn | Ile | Asn | 805 | 810 | 815 | |
| Pro | Pro | Pro | Lys | Arg | Lys | Ile | Leu | Ile | Val | Val | Pro | Glu | Ile | Phe | Leu | 820 | 825 | 830 | |
| Pro | Ser | Glu | Asp | Glu | Cys | Gly | Asp | Val | Leu | Val | Met | Arg | Lys | Asn | Ser | 835 | 840 | 845 | |
| Ser | Pro | Ser | Ser | Ile | Thr | Thr | Tyr | Glu | Thr | Cys | Gln | Thr | Tyr | Glu | Arg | 850 | 855 | 860 | |
| Pro | Ile | Ala | Phe | Thr | Ala | Arg | Ser | Arg | Lys | Leu | Trp | Ile | Asn | Phe | Lys | 865 | 870 | 875 | 880 |
| Thr | Ser | Glu | Ala | Asn | Ser | Ala | Arg | Gly | Phe | Gln | Ile | Pro | Tyr | Val | Thr | 885 | 890 | 895 | |
| Tyr | Asp | Glu | Asp | Tyr | Glu | Gln | Leu | Val | Glu | Asp | Ile | Val | Arg | Asp | Gly | 900 | 905 | 910 | |
| Arg | Leu | Tyr | Ala | Ser | Glu | Asn | His | Gln | Glu | Ile | Leu | Lys | Asp | Lys | Lys | 915 | 920 | 925 | |
| Leu | Ile | Lys | Ala | Phe | Phe | Glu | Val | Leu | Ala | His | Pro | Gln | Asn | Tyr | Phe | 930 | 935 | 940 | |
| Lys | Tyr | Thr | Glu | Lys | His | Lys | Glu | Met | Leu | Pro | Lys | Ser | Phe | Ile | Lys | 945 | 950 | 955 | 960 |

Leu Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr Lys
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<210> 15

<211> 3177

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

CG55096-04

<400> 15

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| gagaccggcc | ccggcggctg | ggccgccagt | agctccagcc | atgggctcgg | ggcgcgtaac | 120 |
| cgggctctgc | ctgcttgccc | tgctggccca | cgcccgccgc | gcccagtaca | gcaaagccgc | 180 |
| gcaagatgtg | gatgagtgtg | tggaggggac | tgacaactgc | cacatcgatg | ctatctgcca | 240 |
| gaacaccccg | aggtcataca | agtgcacatg | caagtctggc | tacacagggg | acggcaaaca | 300 |
| ctgcaaagac | gtggatgagt | gcgagcgaga | ggataatgca | ggttggtgtg | atgactgtgt | 360 |
| caacatccct | ggcaattacc | ggtgtacctg | ctatgatgga | ttccacctgg | cacatgacgg | 420 |
| acacaactgt | ctggatgtgg | acgagtgtgc | cgagggcaac | ggcggctgtc | agcagagctg | 480 |
| tgtcaacatg | atgggcagct | atgagtgccca | ctgccgggaa | ggcttcttcc | tcagcgacaa | 540 |
| ccagcatacc | tgtatccagc | ggccagaaga | aggaatgaat | tgcatgaaca | agaaccacgg | 600 |
| ctgtgcccac | atttgccggg | agacacccaa | gggggggtatt | gcctgtgaat | gccgtcctgg | 660 |
| ctttgagctt | accaagaacc | aacgggactg | taaattgaca | tgcaactatg | gtaacggcgg | 720 |
| ctgccagcac | acgtgtgatg | acacagagca | gggtccccgg | tgccgctgcc | atatcaagtt | 780 |
| tgtgctccat | accgacggga | agacatgcat | cggggaaagg | cggctagagc | agcacatccc | 840 |
| cactcaagcc | gtttctaatg | agacctgtgc | tgtcaacaac | gggggctgtg | acagtaagtg | 900 |
| ccatgatgca | gcgactgggt | tccactgcac | ctgcctgtg | ggcttcatgc | tgacccata | 960 |
| caggaagacg | tgcaaagata | tagatgagt | cgctttaaac | aacgggggct | gtgaccatat | 1020 |
| ttgccgcaac | acagtgggca | gcttcgaatg | cagttgcaag | aaaggctata | agcttctcat | 1080 |
| caatgagagg | aactgccagg | atatagacga | gcgttccttt | gatcgaacct | gtgaccacat | 1140 |
| atgtgtcaac | acaccaggaa | gcttccagtg | tctctgccat | cgtggctacc | tgttgatagg | 1200 |
| tatcacccac | tgtggggatg | tggatgaatg | cagcatcaac | cggggagggt | gccgctttgg | 1260 |
| ctgcatcaac | actcctggca | gctaccagtg | tacctgcccc | gcaggccagg | gtcggctgca | 1320 |
| ctggaatggc | aaagattgca | cagagccact | gaagtgtcag | ggcagtcctg | gggcctcgaa | 1380 |
| agccatgctc | agctgcaacc | ggtctggcaa | gaaggacacc | tgtgccctga | cctgtccctc | 1440 |
| caggggccga | tttttgccag | agtctgagaa | tggcttcacg | gtgagctgtg | ggacccccag | 1500 |
| ccccagggct | gctccagccc | gagctggcca | caatgggaac | agcaccaact | ccaaccactg | 1560 |
| ccatgaggct | gcagtgtgtg | ccattaaaca | acgggcctcc | ttcaagatca | aggatgccaa | 1620 |
| atgccgtttg | cacctgcgaa | acaaaggcaa | aacagaggag | gctggcagaa | tcacagggcc | 1680 |
| agggtggtgc | ccctgctctg | aatgccaggt | caccttcac | caccttaagt | gtgactcctc | 1740 |
| tcggaagggc | aagggccgac | gggcccggac | ccctccaggc | aaagagggtc | caagggtcac | 1800 |
| cctggaactg | gaggcagagg | tcagagccga | agaaaccaca | gccagctgtg | ggctgcctcg | 1860 |
| cctccgacag | cgaatggaac | ggcggctgaa | aggatccctg | aagatgctca | gaaagtccat | 1920 |
| caaccaggag | cgcttcctgc | tgcgcctggc | aggccttgat | tatgagctgg | cccacaagcc | 1980 |
| gggcctggta | gccggggagc | gagcagagcc | gatggagtc | tgtaggcccg | ggcagcaccg | 2040 |
| tgctggggacc | aagtgtgtca | gctgcccgc | gggaacgtat | taccacggcc | agacggagca | 2100 |
| gtgtgtgcc | tgcccagcgg | gcaccttcca | ggagagagaa | gggcagctct | cctgcgacct | 2160 |
| ttgccctggg | agtgatgcc | acgggcctct | tggagccacc | aacgtcacca | cgtgtgcagg | 2220 |
| tcagtgccca | cctggccaac | actctgtaga | tgggttcaag | ccctgtcagc | catgcccacg | 2280 |
| tggcacctac | caacctgaag | caggacggac | cctatgcttc | ccttggtgtg | ggggcctcac | 2340 |
| caccaagcat | gaaggggcca | tttcttcca | agactgtgac | accaaagtcc | agtgtccccc | 2400 |
| agggcactac | tacaacacca | gcattccacc | ctgtattcgc | tgtgccatgg | gctccatcca | 2460 |
| gcccgaactc | cgtcagaact | tctgcagccg | ctgtccagga | aacacaagca | cagactttga | 2520 |
| tggctctacc | agtgtggccc | aatgcaagaa | tcgtcagtg | ggtggggagc | tgggtgagtt | 2580 |
| cactggctat | attgagtccc | ccaactaccc | gggcaactac | ccagctgggtg | tggagtgc | 2640 |

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cattaccact tatgagacct gccagacctt cgagcggtccc attgccttca ctgcccgttc 2820
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<210> 16

<211> 1009

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

CG55096-04

<400> 16

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His Ala Arg Ala Ala Gln Tyr Ser Lys Ala Ala Gln Asp Val Asp Glu
      20              25              30

Cys Val Glu Gly Thr Asp Asn Cys His Ile Asp Ala Ile Cys Gln Asn
      35              40              45

Thr Pro Arg Ser Tyr Lys Cys Ile Cys Lys Ser Gly Tyr Thr Gly Asp
      50              55              60

Gly Lys His Cys Lys Asp Val Asp Glu Cys Glu Arg Glu Asp Asn Ala
      65              70              75              80

Gly Cys Val His Asp Cys Val Asn Ile Pro Gly Asn Tyr Arg Cys Thr
      85              90              95

Cys Tyr Asp Gly Phe His Leu Ala His Asp Gly His Asn Cys Leu Asp
      100             105             110

Val Asp Glu Cys Ala Glu Gly Asn Gly Gly Cys Gln Gln Ser Cys Val
      115             120             125

Asn Met Met Gly Ser Tyr Glu Cys His Cys Arg Glu Gly Phe Phe Leu
      130             135             140

Ser Asp Asn Gln His Thr Cys Ile Gln Arg Pro Glu Glu Gly Met Asn
      145             150             155             160

Cys Met Asn Lys Asn His Gly Cys Ala His Ile Cys Arg Glu Thr Pro
      165             170             175

Lys Gly Gly Ile Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Thr Lys
      180             185             190

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Gln | Arg | Asp | Cys | Lys | Leu | Thr | Cys | Asn | Tyr | Gly | Asn | Gly | Gly | Cys | |
| | | 195 | | | | | | 200 | | | | | 205 | | | |
| Gln | His | Thr | Cys | Asp | Asp | Thr | Glu | Gln | Gly | Pro | Arg | Cys | Gly | Cys | His | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| Ile | Lys | Phe | Val | Leu | His | Thr | Asp | Gly | Lys | Thr | Cys | Ile | Gly | Glu | Arg | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Arg | Leu | Glu | Gln | His | Ile | Pro | Thr | Gln | Ala | Val | Ser | Asn | Glu | Thr | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ala | Val | Asn | Asn | Gly | Gly | Cys | Asp | Ser | Lys | Cys | His | Asp | Ala | Ala | Thr | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Gly | Val | His | Cys | Thr | Cys | Pro | Val | Gly | Phe | Met | Leu | Gln | Pro | Asp | Arg | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Lys | Thr | Cys | Lys | Asp | Ile | Asp | Glu | Cys | Arg | Leu | Asn | Asn | Gly | Gly | Cys | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| Asp | His | Ile | Cys | Arg | Asn | Thr | Val | Gly | Ser | Phe | Glu | Cys | Ser | Cys | Lys | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Lys | Gly | Tyr | Lys | Leu | Leu | Ile | Asn | Glu | Arg | Asn | Cys | Gln | Asp | Ile | Asp | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Glu | Arg | Ser | Phe | Asp | Arg | Thr | Cys | Asp | His | Ile | Cys | Val | Asn | Thr | Pro | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Gly | Ser | Phe | Gln | Cys | Leu | Cys | His | Arg | Gly | Tyr | Leu | Leu | Tyr | Gly | Ile | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Thr | His | Cys | Gly | Asp | Val | Asp | Glu | Cys | Ser | Ile | Asn | Arg | Gly | Gly | Cys | |
| | | 370 | | | | 375 | | | | | 380 | | | | | |
| Arg | Phe | Gly | Cys | Ile | Asn | Thr | Pro | Gly | Ser | Tyr | Gln | Cys | Thr | Cys | Pro | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Ala | Gly | Gln | Gly | Arg | Leu | His | Trp | Asn | Gly | Lys | Asp | Cys | Thr | Glu | Pro | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Leu | Lys | Cys | Gln | Gly | Ser | Pro | Gly | Ala | Ser | Lys | Ala | Met | Leu | Ser | Cys | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Asn | Arg | Ser | Gly | Lys | Lys | Asp | Thr | Cys | Ala | Leu | Thr | Cys | Pro | Ser | Arg | |
| | | | 435 | | | | 440 | | | | | 445 | | | | |
| Ala | Arg | Phe | Leu | Pro | Glu | Ser | Glu | Asn | Gly | Phe | Thr | Val | Ser | Cys | Gly | |
| | | 450 | | | | 455 | | | | | 460 | | | | | |
| Thr | Pro | Ser | Pro | Arg | Ala | Ala | Pro | Ala | Arg | Ala | Gly | His | Asn | Gly | Asn | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Ser | Thr | Asn | Ser | Asn | His | Cys | His | Glu | Ala | Ala | Val | Leu | Ser | Ile | Lys | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |

Gln Arg Ala Ser Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu
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 Arg Asn Lys Gly Lys Thr Glu Glu Ala Gly Arg Ile Thr Gly Pro Gly
 515 520 525
 Gly Ala Pro Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys
 530 535 540
 Asp Ser Ser Arg Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly
 545 550 555 560
 Lys Glu Val Thr Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala
 565 570 575
 Glu Glu Thr Thr Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met
 580 585 590
 Glu Arg Arg Leu Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn
 595 600 605
 Gln Asp Arg Phe Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala
 610 615 620
 His Lys Pro Gly Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser
 625 630 635 640
 Cys Arg Pro Gly Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro
 645 650 655
 Gln Gly Thr Tyr Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro
 660 665 670
 Ala Gly Thr Phe Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys
 675 680 685
 Pro Gly Ser Asp Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr
 690 695 700
 Cys Ala Gly Gln Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys
 705 710 715 720
 Pro Cys Gln Pro Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg
 725 730 735
 Thr Leu Cys Phe Pro Cys Gly Gly Gly Leu Thr Thr Lys His Glu Gly
 740 745 750
 Ala Ile Ser Phe Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly
 755 760 765
 His Tyr Tyr Asn Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly
 770 775 780
 Ser Tyr Gln Pro Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly
 785 790 795 800

Asn Thr Ser Thr Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys
 805 810 815
 Asn Arg Gln Cys Gly Gly Glu Leu Gly Glu Phe Thr Gly Tyr Ile Glu
 820 825 830
 Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Gly Val Glu Cys Ile Trp
 835 840 845
 Asn Ile Asn Pro Pro Pro Lys Arg Lys Ile Leu Ile Val Val Pro Glu
 850 855 860
 Ile Phe Leu Pro Ser Glu Asp Glu Cys Gly Asp Val Leu Val Met Arg
 865 870 875 880
 Lys Asn Ser Ser Pro Ser Ser Ile Thr Thr Tyr Glu Thr Cys Gln Thr
 885 890 895
 Tyr Glu Arg Pro Ile Ala Phe Thr Ala Arg Ser Arg Lys Leu Trp Ile
 900 905 910
 Asn Phe Lys Thr Ser Glu Ala Asn Ser Ala Arg Gly Phe Gln Ile Pro
 915 920 925
 Tyr Val Thr Tyr Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val
 930 935 940
 Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
 945 950 955 960
 Asp Lys Lys Leu Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln
 965 970 975
 Asn Tyr Phe Lys Tyr Thr Glu Lys His Lys Glu Met Leu Pro Lys Ser
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 Phe Ile Lys Leu Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr
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Lys

<210> 17

<211> 1709

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
10327789.0.16

<400> 17

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 aaaaatagaa tggatctatt ggaaaaacca taaatcatta ttgtcttact tcctaattga 360

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<210> 18

<211> 344

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
10327789.0.16

<400> 18

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Ala Gln His Thr Thr Gly Arg Ile Phe Glu Ser Glu Val Arg Tyr Gln
      20             25             30

Cys Asn Pro Gly Tyr Lys Ser Val Gly Ser Pro Val Phe Val Cys Gln
      35             40             45

Ala Asn Arg His Trp His Ser Glu Ser Pro Leu Met Cys Val Pro Leu
      50             55             60

Asp Cys Gly Lys Pro Pro Pro Ile Gln Asn Gly Phe Met Lys Gly Glu
      65             70             75             80

Asn Phe Glu Val Gly Ser Lys Val Gln Phe Phe Cys Asn Glu Gly Tyr
      85             90             95

Glu Leu Val Gly Asp Ser Ser Trp Thr Cys Gln Lys Ser Gly Lys Trp
      100            105            110

Asn Lys Lys Ser Asn Pro Lys Cys Met Pro Ala Lys Cys Pro Glu Pro
      115            120            125

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Pro Leu Leu Glu Asn Gln Leu Val Leu Lys Glu Leu Thr Thr Glu Val
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Gly Val Val Thr Phe Ser Cys Lys Glu Gly His Val Leu Gln Gly Pro
 145 150 155 160

Ser Val Leu Lys Cys Leu Pro Ser Gln Gln Trp Asn Asp Ser Phe Pro
 165 170 175

Val Cys Lys Ile Val Leu Cys Thr Pro Pro Pro Leu Ile Ser Phe Gly
 180 185 190

Val Pro Ile Pro Ser Ser Ala Leu His Phe Gly Ser Thr Val Lys Tyr
 195 200 205

Ser Cys Val Gly Gly Phe Phe Leu Arg Gly Asn Ser Thr Thr Leu Cys
 210 215 220

Gln Pro Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val
 225 230 235 240

Glu Cys Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln
 245 250 255

Gly Leu Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe
 260 265 270

Glu Leu Val Gly Asn Thr Thr Thr Leu Cys Gly Glu Asn Gly His Trp
 275 280 285

Leu Gly Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys
 290 295 300

Glu Ile Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln
 305 310 315 320

Thr Val Thr Tyr Ser Cys Asn Arg Gly Phe Arg Leu Glu Gly Ser Gln
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Cys Leu Asp Leu Phe Arg Asp Arg
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<210> 19

<211> 1952

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 10327789.0.140

<400> 19

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<212> PRT

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10327789.0.140

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Ala Tyr Ser Cys Asn Lys Gly Phe Tyr Ile Lys Gly Glu Lys Lys Ser
35 40 45

Thr Cys Glu Ala Thr Gly Gln Trp Ser Ser Pro Ile Pro Thr Cys His
50 55 60

Pro Val Ser Cys Gly Glu Pro Pro Lys Val Glu Asn Gly Phe Leu Glu
65 70 75 80

His Thr Thr Gly Arg Ile Phe Glu Ser Glu Val Arg Tyr Gln Cys Asn
85 90 95

| | | | |
|---|-----|-----|-----|
| Pro Gly Tyr Lys Ser Val Gly Ser Pro Val Phe Val Cys Gln Ala Asn | 100 | 105 | 110 |
| Arg His Trp His Ser Glu Ser Pro Leu Met Cys Val Pro Leu Asp Cys | 115 | 120 | 125 |
| Gly Lys Pro Pro Pro Ile Gln Asn Gly Phe Met Lys Gly Glu Asn Phe | 130 | 135 | 140 |
| Glu Val Gly Ser Lys Val Gln Phe Phe Cys Asn Glu Gly Tyr Glu Leu | 145 | 150 | 155 |
| Val Gly Asp Ser Ser Trp Thr Cys Gln Lys Ser Gly Lys Trp Asn Lys | 165 | 170 | 175 |
| Lys Ser Asn Pro Lys Cys Met Pro Ala Lys Cys Pro Glu Pro Pro Leu | 180 | 185 | 190 |
| Leu Glu Asn Gln Leu Val Leu Lys Glu Leu Thr Thr Glu Val Gly Val | 195 | 200 | 205 |
| Val Thr Phe Ser Cys Lys Glu Gly His Val Leu Gln Gly Pro Ser Val | 210 | 215 | 220 |
| Leu Lys Cys Leu Pro Ser Gln Gln Trp Asn Asp Ser Phe Pro Val Cys | 225 | 230 | 235 |
| Lys Ile Val Leu Cys Thr Pro Pro Pro Leu Ile Ser Phe Gly Val Pro | 245 | 250 | 255 |
| Ile Pro Ser Ser Ala Leu His Phe Gly Ser Thr Val Lys Tyr Ser Cys | 260 | 265 | 270 |
| Val Gly Gly Phe Phe Leu Arg Gly Asn Ser Thr Thr Leu Cys Gln Pro | 275 | 280 | 285 |
| Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val Glu Cys | 290 | 295 | 300 |
| Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln Gly Leu | 305 | 310 | 315 |
| Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe Glu Leu | 325 | 330 | 335 |
| Val Gly Asn Thr Thr Thr Leu Cys Gly Glu Asn Gly His Trp Leu Gly | 340 | 345 | 350 |
| Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys Glu Ile | 355 | 360 | 365 |
| Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln Thr Val | 370 | 375 | 380 |
| Thr Tyr Ser Cys Asn Arg Gly Phe Arg Leu Glu Gly Ser Gln Cys Leu | 385 | 390 | 395 |
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Asp Leu Phe Arg Asp Arg
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| | | | | | | |
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| ccacgctgtg | aagccatttc | atgcaaaaag | ccaaatccag | tcatgaatgg | atccatcaaa | 2580 |
| ggaagcaact | acacatacct | gagcacgttg | tactatgagt | gtgaccccg | atatgtgctg | 2640 |
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| ttagaaagga | atgtaaatga | cctgatggag | ctgaaaaaca | caacacgaga | acttcacaa | 5580 |
| gcaacaacaa | aacaaggcca | acattccagt | tcaggaaatc | cagagaaccc | cagaaagata | 5640 |
| ctccatgaga | agatcaaccc | caagacacat | aatcctcagg | ttctccaaga | aatctcatgt | 5700 |
| ggtccaccag | ctcacgtaga | aaatgcaatt | gctcaggcgg | tacattatca | atatggagac | 5760 |
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10327789_1

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```

```

Ser Glu Pro Gly Val Gly Tyr Ser Leu Val Val Arg Arg Phe Leu Ser
    35              40              45

```

```

Arg Ser Glu Lys Arg Asn Ile Arg Val Gly Val Thr Arg Phe Ser Ser
    50              55              60

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```

Tyr Thr Leu Ala Gly Leu Asp Thr Ile Glu Cys Leu Ala Asp Gly Lys
    65              70              75              80

```

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Trp Ser Arg Ser Asp Gln Gln Cys Leu Ala Val Ser Cys Asp Glu Pro
          85              90              95

```

```

Pro Ile Val Asp His Ala Ser Pro Glu Thr Ala His Arg Leu Phe Gly
    100              105              110

```

```

Asp Ile Ala Phe Tyr Tyr Cys Ser Asp Gly Tyr Ser Leu Ala Asp Asn
    115              120              125

```

```

Ser Gln Leu Leu Cys Asn Ala Gln Gly Lys Trp Val Pro Pro Glu Gly
    130              135              140

```

```

Gln Asp Met Pro Arg Cys Ile Ala His Phe Cys Glu Lys Pro Pro Ser
    145              150              155              160

```

```

Val Ser Tyr Ser Ile Leu Glu Ser Val Ser Lys Ala Lys Phe Ala Ala
    165              170              175

```

```

Gly Ser Val Val Ser Phe Lys Cys Met Glu Gly Phe Val Leu Asn Thr
    180              185              190

```

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Lys | Ile | Glu | Cys | Met | Arg | Gly | Gly | Gln | Trp | Asn | Pro | Ser | Pro | 195 | 200 | 205 |
| Met | Ser | Ile | Gln | Cys | Ile | Pro | Val | Arg | Cys | Gly | Glu | Pro | Pro | Ser | Ile | 210 | 215 | 220 |
| Met | Asn | Gly | Tyr | Ala | Ser | Gly | Ser | Asn | Tyr | Ser | Phe | Gly | Ala | Met | Val | 225 | 230 | 235 |
| Ala | Tyr | Ser | Cys | Asn | Lys | Gly | Phe | Tyr | Ile | Lys | Gly | Glu | Lys | Lys | Ser | 245 | 250 | 255 |
| Thr | Cys | Glu | Ala | Thr | Gly | Gln | Trp | Ser | Ser | Pro | Ile | Pro | Thr | Cys | His | 260 | 265 | 270 |
| Pro | Val | Ser | Cys | Gly | Glu | Pro | Pro | Lys | Val | Glu | Asn | Gly | Phe | Leu | Glu | 275 | 280 | 285 |
| His | Thr | Thr | Gly | Arg | Ile | Phe | Glu | Ser | Glu | Val | Arg | Tyr | Gln | Cys | Asn | 290 | 295 | 300 |
| Pro | Gly | Tyr | Lys | Ser | Val | Gly | Ser | Pro | Val | Phe | Val | Cys | Gln | Ala | Asn | 305 | 310 | 315 |
| Arg | His | Trp | His | Ser | Glu | Ser | Pro | Leu | Met | Cys | Val | Pro | Leu | Asp | Cys | 325 | 330 | 335 |
| Gly | Lys | Pro | Pro | Pro | Ile | Gln | Asn | Gly | Phe | Met | Lys | Gly | Glu | Asn | Phe | 340 | 345 | 350 |
| Glu | Val | Gly | Ser | Lys | Gly | Gln | Phe | Phe | Cys | Asn | Glu | Gly | Leu | Xaa | Ser | 355 | 360 | 365 |
| Phe | Val | Gly | Asp | Ser | Ser | Trp | Thr | Cys | Gln | Lys | Ser | Gly | Lys | Trp | Asn | 370 | 375 | 380 |
| Lys | Lys | Ser | Asn | Pro | Lys | Cys | Met | Pro | Ala | Lys | Cys | Pro | Glu | Pro | Pro | 385 | 390 | 395 |
| Leu | Leu | Glu | Asn | Gln | Leu | Val | Leu | Lys | Glu | Leu | Thr | Thr | Glu | Val | Gly | 405 | 410 | 415 |
| Val | Val | Thr | Phe | Ser | Cys | Lys | Glu | Arg | His | Val | Leu | Gln | Gly | Pro | Ser | 420 | 425 | 430 |
| Val | Leu | Lys | Cys | Leu | Pro | Ser | Gln | Gln | Trp | Asn | Asp | Ser | Phe | Pro | Val | 435 | 440 | 445 |
| Cys | Lys | Ile | Val | Leu | Cys | Thr | Pro | Pro | Pro | Leu | Ile | Ser | Phe | Gly | Val | 450 | 455 | 460 |
| Pro | Ile | Pro | Ser | Ser | Ala | Leu | His | Phe | Gly | Ser | Thr | Val | Lys | Tyr | Ser | 465 | 470 | 475 |
| Cys | Val | Gly | Gly | Phe | Phe | Leu | Arg | Gly | Asn | Ser | Thr | Thr | Leu | Cys | Gln | 485 | 490 | 495 |

Pro Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val Glu
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 Cys Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln Gly
 515 520 525
 Leu Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe Glu
 530 535 540
 Leu Val Gly Asn Thr Thr Thr Leu Cys Gly Glu Asn Gly His Trp Leu
 545 550 555 560
 Gly Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys Glu
 565 570 575
 Ile Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln Thr
 580 585 590
 Val Thr Tyr Ser Cys Asn Arg Gly Phe Arg Leu Glu Gly Pro Ser Ala
 595 600 605
 Leu Thr Cys Leu Glu Thr Gly Asp Trp Asp Val Asp Ala Pro Ser Cys
 610 615 620
 Asn Ala Ile His Cys Asp Ser Pro Gln Pro Ile Glu Asn Gly Phe Val
 625 630 635 640
 Glu Gly Ala Asp Tyr Ser Tyr Gly Ala Ile Ile Ile Tyr Ser Cys Phe
 645 650 655
 Pro Gly Phe Gln Val Ala Gly His Ala Met Gln Thr Cys Glu Glu Ser
 660 665 670
 Gly Trp Ser Ser Ser Ile Pro Thr Cys Met Pro Ile Asp Cys Gly Leu
 675 680 685
 Pro Pro His Ile Asp Phe Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln
 690 695 700
 Gly Tyr Phe Glu Gln Glu Asp Asp Met Met Glu Val Pro Tyr Val Thr
 705 710 715 720
 Pro His Pro Pro Tyr His Leu Gly Ala Val Ala Lys Thr Trp Glu Asn
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 Thr Lys Glu Ser Pro Ala Thr His Ser Ser Asn Phe Leu Tyr Gly Thr
 740 745 750
 Met Val Ser Tyr Thr Cys Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro
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 Val Leu Ile Cys Gln Glu Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser
 770 775 780
 Cys Ile Ser Ile Glu Cys Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe
 785 790 795 800

Leu Arg Phe Thr Glu Thr Ser Met Gly Ser Ala Val Gln Tyr Ser Cys
 805 810 815
 Lys Pro Gly His Ile Leu Ala Gly Ser Asp Leu Arg Leu Cys Leu Glu
 820 825 830
 Asn Arg Lys Trp Ser Gly Ala Ser Pro Arg Cys Glu Ala Ile Ser Cys
 835 840 845
 Lys Lys Pro Asn Pro Val Met Asn Gly Ser Ile Lys Gly Ser Asn Tyr
 850 855 860
 Thr Tyr Leu Ser Thr Leu Tyr Tyr Glu Cys Asp Pro Gly Tyr Val Leu
 865 870 875 880
 Asn Gly Thr Glu Arg Arg Thr Cys Gln Asp Asp Lys Asn Trp Asp Glu
 885 890 895
 Asp Glu Pro Ile Cys Ile Pro Val Asp Cys Ser Ser Pro Pro Val Ser
 900 905 910
 Ala Asn Gly Gln Val Arg Gly Asp Glu Tyr Thr Phe Gln Lys Glu Ile
 915 920 925
 Glu Tyr Thr Cys Asn Glu Gly Phe Leu Leu Glu Gly Ala Arg Ser Arg
 930 935 940
 Val Cys Leu Ala Asn Gly Ser Trp Ser Gly Ala Thr Pro Asp Cys Val
 945 950 955 960
 Pro Val Arg Cys Ala Thr Pro Pro Gln Leu Ala Asn Gly Val Thr Glu
 965 970 975
 Gly Leu Asp Tyr Gly Phe Met Lys Glu Val Thr Phe His Cys His Glu
 980 985 990
 Gly Tyr Ile Leu His Gly Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly
 995 1000 1005
 Asn Trp Asp Ala Glu Ile Pro Leu Cys Lys Pro Val Asn Cys Gly Pro
 1010 1015 1020
 Pro Glu Asp Leu Ala His Gly Phe Pro Asn Gly Phe Ser Phe Ile His
 1025 1030 1035 1040
 Gly Gly His Ile Gln Tyr Gln Cys Phe Pro Gly Tyr Lys Leu His Gly
 1045 1050 1055
 Asn Ser Ser Arg Arg Cys Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser
 1060 1065 1070
 Pro Ser Cys Leu Pro Cys Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly
 1075 1080 1085
 Thr Val Asn Gly Thr Asp Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln
 1090 1095 1100

Cys Phe Lys Gly Phe Lys Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu
 1105 1110 1115 1120
 Ala Asp Gly Gln Trp Ser Ser Gly Phe Pro His Cys Glu His Thr Ser
 1125 1130 1135
 Cys Gly Ser Leu Pro Met Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser
 1140 1145 1150
 Ser Trp Lys Glu Asn Val Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val
 1155 1160 1165
 Ile Gln Gly Ser Ser Asp Leu Ile Cys Thr Glu Lys Gly Val Trp Ser
 1170 1175 1180
 Gln Pro Tyr Pro Val Cys Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser
 1185 1190 1195 1200
 Val Ala Asn Ala Val Ala Thr Gly Glu Ala His Thr Tyr Glu Ser Glu
 1205 1210 1215
 Val Lys Leu Arg Cys Leu Glu Gly Tyr Thr Met Asp Thr Asp Thr Asp
 1220 1225 1230
 Thr Phe Thr Cys Gln Lys Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser
 1235 1240 1245
 Cys Ser Pro Lys Lys Cys Pro Leu Pro Glu Asn Ile Thr His Ile Leu
 1250 1255 1260
 Val His Gly Asp Asp Phe Ser Val Asn Arg Gln Val Ser Val Ser Cys
 1265 1270 1275 1280
 Ala Glu Gly Tyr Thr Phe Glu Gly Val Asn Ile Ser Val Cys Gln Leu
 1285 1290 1295
 Asp Gly Thr Trp Glu Pro Pro Phe Ser Asp Glu Ser Cys Ser Pro Val
 1300 1305 1310
 Ser Cys Gly Lys Pro Glu Ser Pro Glu His Gly Phe Val Val Gly Ser
 1315 1320 1325
 Lys Tyr Thr Phe Glu Ser Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr
 1330 1335 1340
 Glu Leu Glu Asn Leu Ala Val Asn Pro Ser Gly Pro Gly Leu Phe Leu
 1345 1350 1355 1360
 Val Asp Arg Thr Leu Ser Cys Arg Ser Glu Leu Ala Arg Gly Pro Ile
 1365 1370 1375
 Gln Thr Leu Phe Ala Trp Val Ser Ala Ala Glu Gly Ala Glu Gln Arg
 1380 1385 1390
 Ile Leu Val Asn Arg Lys Cys Cys Cys Leu Ile Ile Pro Leu Glu Val
 1395 1400 1405

Leu Ser Gln Arg Asn Thr Arg Pro Cys Glu Val Ser Val Arg Pro Tyr
 1410 1415 1420
 Trp Gly Gly Asn Arg Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser
 1425 1430 1435 1440
 Gly Gly Val Ala Ile Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu
 1445 1450 1455
 Phe Leu Asn Gly Lys Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn
 1460 1465 1470
 Val Val Tyr Ser Cys Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu
 1475 1480 1485
 Ala His Cys Thr Glu Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys
 1490 1495 1500
 Lys Pro Asn Pro Cys Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu
 1505 1510 1515 1520
 Leu Ser Glu Lys Glu Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys
 1525 1530 1535
 Arg Glu Gly Phe Leu Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro
 1540 1545 1550
 Asp Glu Thr Trp Thr Gln Thr Ser Ala Lys Cys Glu Arg Arg Tyr Thr
 1555 1560 1565
 Gln Gln Pro Lys Ser Leu Asn Phe Gln Leu Ala Ala Tyr Cys Ser Ile
 1570 1575 1580
 Arg Met Phe Ile Leu Arg Gly Gly Val Gln Asp Gly Gln Leu Glu Thr
 1585 1590 1595 1600
 Ala Val Ala Gly Ala Ser His Arg Glu Glu Gln Lys Gln Lys Arg Glu
 1605 1610 1615
 Lys Ala Arg Trp Tyr Asn Gly Pro Pro Gly Ser His Met Gly Gln Ala
 1620 1625 1630
 Glu Leu Pro Pro Pro Ala Lys Gly Gly Gly Pro Pro Cys Gly Asn Phe
 1635 1640 1645
 Ser Asn Ser Ser Gln Gly Phe Met Asn Arg Pro Leu Ile Ser Leu Arg
 1650 1655 1660
 Trp Ser Pro Trp Gly Ser Met Trp Pro Trp Ser Pro Gln Ile Ser Arg
 1665 1670 1675 1680
 Leu Ser Pro Ser Pro Ala Gly Ser Glu Glu Ser Arg Gln Ala Gly Leu
 1685 1690 1695
 Val Gly Phe Pro Thr Ala Gln Phe Thr Cys Ser Ala Lys Gly Gln Leu
 1700 1705 1710

Glu Arg Phe Val Lys Arg Val Pro Asp Pro Met Pro Pro Asp Trp Asp
 1715 1720 1725

Glu Thr Pro Pro Gln Gln Gly Ser Arg Met Arg Pro Pro His Asn Arg
 1730 1735 1740

Gly His Gln Thr Pro Tyr Thr Arg Val Phe Leu Leu Ala Ser Gly Gln
 1745 1750 1755 1760

Cys Pro Ser Gly Thr Glu Leu Pro Glu Glu Arg Ala Gly Ser His Leu
 1765 1770 1775

Cys Cys Ser Ala Ala Ser Ala Gly Lys Ala Gln Asn Trp Ala Glu Ala
 1780 1785 1790

Arg Ile Asp Glu Leu Lys Glu Val Gly Phe Arg Lys Trp Val Ile Met
 1795 1800 1805

Lys Phe Ala Glu Leu Lys Glu His Val Leu Asn Gln Cys Lys Asp Ala
 1810 1815 1820

Lys Asn Gln Asp Lys Thr Leu Gln Asp Pro Leu Thr Arg Ile Thr Ser
 1825 1830 1835 1840

Leu Glu Arg Asn Val Asn Asp Leu Met Glu Leu Lys Asn Thr Thr Arg
 1845 1850 1855

Glu Leu His Asn Ala Thr Thr Lys Gln Gly Gln His Ser Ser Ser Gly
 1860 1865 1870

Asn Pro Glu Asn Pro Ser Lys Ile Leu His Glu Lys Ile Asn Pro Lys
 1875 1880 1885

Thr His Asn Pro Gln Val Leu Gln Glu Ile Ser Cys Gly Pro Pro Ala
 1890 1895 1900

His Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln Tyr Gly Asp
 1905 1910 1915 1920

Met Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu Gly Phe Leu
 1925 1930 1935

Arg Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro Pro Ile Cys
 1940 1945 1950

Arg Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Gly Ile Cys Gln Arg
 1955 1960 1965

Pro Asn Ala Cys Ser Cys Pro Glu Gly Trp Met Gly Arg Leu Cys Glu
 1970 1975 1980

Glu Pro Ile Cys Ile Leu Pro Cys Leu Asn Gly Gly Arg Cys Val Ala
 1985 1990 1995 2000

Pro Tyr Gln Cys Asp Cys Pro Pro Gly Trp Thr Gly Ser Arg Cys His
 2005 2010 2015

Thr Gly Arg Pro Leu Ser Trp Phe Val Phe Leu Val Ala Gln Ala His
 2020 2025 2030

Glu Thr Pro Glu Asp Ile Glu Glu Cys Asp Leu Asp Ser Glu Val Val
 2035 2040 2045

Ala Lys
 2050

<210> 23
 <211> 2216
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 AC016030_A.0.82

<400> 23
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 aggagcccg ggcctctcg ccgctccccg cgcgcgcgtc cgcacctccc caccgcccgc 180
 cgcccgcgcg ccgcccgcgcg caaagcatga gtgagccgcg tctctgcagc tgcgcggggc 240
 gcgaatggca ggctgtttcc gcggagtaaa aggtggcgcc ggtcagtggt cgtttccaat 300
 gacggacatt aaccagactg tcagatcctg gggagtcgcg agccccgagt ttggagtttt 360
 ttccccccac aacgtcacag tccgaactgc agagggaaaag gaaggcggca ggaaggcgaa 420
 gctcgggctc cggcacgtag ttgggaaact tgccgggtcct agaagtcgcc tccccgcctt 480
 gccggccgcc cttgcagccc cgagccgagc agcaaagtga gacattgtgc gcctgccaga 540
 tccgcccggc gcggaccggg gctgcctcgg aaacacagag gggctcttct tcgcccgcga 600
 tataattagc ctgcacacaa agggagcagc tgaatggagg ttgtcactct ctggaaaagg 660
 atttctgacc gagcgttcc aatggacatt ctccagtcct tctggaaaga ttctcgctaa 720
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 cccacaacct gtccggcctg ctgggcttgt ccctgcgcta caacagcctc tggagctgc 960
 gcgcccggca gttcacgggg ttaatgcagc tcacgtgggt ctatctggat cacaatcaca 1020
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 gtgctaccg gagctgcggg ggcgtctcca cagcgaacca tgaagttgaa ggacacaaaa 1140
 tcaaggccaa agcagtcagg ctgtggcaaa ttccagacaa agggaatcaa agttgtggga 1200
 aaatggaagg aaatggacag atggatgact tgggtgtgct tgaggaattg acagattacc 1260
 agttggtctc ccctgccaa aatccctcca gtctcttctc aaaggaagca cccaagagaa 1320
 aggcacaagc tgtttcagaa gaagaggagg agggaggagg aaagtctagc tcaccaaaaga 1380
 aaaagatcaa gttgaagaaa agtaaaaatg tagcaactga aggaaccagt acccagaaaag 1440
 aatttgaaat gaaagatcct gagctggagg cccaggggaga tgacatgggt tgtgatgatc 1500
 cggagggtgg ggagatgaca tcagaaaacc tgggtccaaac tgctccaaaa aagaagaaaa 1560
 ataaagggaa aaaagggttg gagccttctc agagcactgc tgccaagggt cccaaaaaag 1620
 cgaagacatg gattcctgaa gttcatgac agaaagcaga tgtgtcagct tgggaaggac 1680
 tgtttgttcc caggccggtt ctccgagcac tcagctttct aggttctct gcacccacac 1740
 caatccaagc cctgaccttg gcacctgcca tccgtgacaa actggacatc cttggggctg 1800
 ctgagacagg aagtgggaaa actcttgctt ttgccatccc aatgattcat gcggtgttgc 1860
 agtggcagaa gaggaatgct gccctcctc caagtaacac cgaagcacca cctggagaga 1920
 ccagaactga ggccggagct gagactagat taccaggcaa ggctgaagct gactctgatg 1980
 cattgcctga cgatactgta attgagagt aagcactgcc cagtgatatt gcagccgagg 2040
 ccagagccaa gactggaggc actgtctcag accaggcggt gctctttgag tgacgatgat 2100
 gctgggtgaag ggccttcttc cctgatcagg gagaaacctg ttcccaaaca gaatgggaat 2160
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<210> 24
 <211> 457
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 AC016030_A.0.82

<400> 24
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 Pro Ala Ala Pro Ser Gly Cys Pro Gln Leu Cys Arg Cys Glu Gly Arg
 35 40 45
 Leu Leu Tyr Cys Glu Ala Leu Asn Leu Thr Glu Ala Pro His Asn Leu
 50 55 60
 Ser Gly Leu Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Ser Glu Leu
 65 70 75 80
 Arg Ala Gly Gln Phe Thr Gly Leu Met Gln Leu Thr Trp Leu Tyr Leu
 85 90 95
 Asp His Asn His Ile Cys Ser Val Gln Gly Asp Ala Phe Gln Lys Leu
 100 105 110
 Arg Arg Val Lys Glu Leu Thr Leu Ser Ala Tyr Arg Ser Cys Gly Gly
 115 120 125
 Val Ser Thr Arg Asn His Glu Val Glu Gly His Lys Ile Lys Ala Lys
 130 135 140
 Ala Val Lys Leu Trp Gln Ile Ser Asp Lys Gly Asn Gln Ser Cys Gly
 145 150 155 160
 Lys Met Glu Gly Asn Gly Gln Met Asp Asp Leu Val Cys Phe Glu Glu
 165 170 175
 Leu Thr Asp Tyr Gln Leu Val Ser Pro Ala Lys Asn Pro Ser Ser Leu
 180 185 190
 Phe Ser Lys Glu Ala Pro Lys Arg Lys Ala Gln Ala Val Ser Glu Glu
 195 200 205
 Glu Glu Glu Glu Glu Gly Lys Ser Ser Ser Pro Lys Lys Lys Ile Lys
 210 215 220
 Leu Lys Lys Ser Lys Asn Val Ala Thr Glu Gly Thr Ser Thr Gln Lys
 225 230 235 240
 Glu Phe Glu Val Lys Asp Pro Glu Leu Glu Ala Gln Gly Asp Asp Met
 245 250 255

Val Cys Asp Asp Pro Glu Ala Gly Glu Met Thr Ser Glu Asn Leu Val
 260 265 270
 Gln Thr Ala Pro Lys Lys Lys Lys Asn Lys Gly Lys Lys Gly Leu Glu
 275 280 285
 Pro Ser Gln Ser Thr Ala Ala Lys Val Pro Lys Lys Ala Lys Thr Trp
 290 295 300
 Ile Pro Glu Val His Asp Gln Lys Ala Asp Val Ser Ala Trp Lys Asp
 305 310 315 320
 Leu Phe Val Pro Arg Pro Val Leu Arg Ala Leu Ser Phe Leu Gly Phe
 325 330 335
 Ser Ala Pro Thr Pro Ile Gln Ala Leu Thr Leu Ala Pro Ala Ile Arg
 340 345 350
 Asp Lys Leu Asp Ile Leu Gly Ala Ala Glu Thr Gly Ser Gly Lys Thr
 355 360 365
 Leu Ala Phe Ala Ile Pro Met Ile His Ala Val Leu Gln Trp Gln Lys
 370 375 380
 Arg Asn Ala Ala Pro Pro Pro Ser Asn Thr Glu Ala Pro Pro Gly Glu
 385 390 395 400
 Thr Arg Thr Glu Ala Gly Ala Glu Thr Arg Leu Pro Gly Lys Ala Glu
 405 410 415
 Ala Glu Ser Asp Ala Leu Pro Asp Asp Thr Val Ile Glu Ser Glu Ala
 420 425 430
 Leu Pro Ser Asp Ile Ala Ala Glu Ala Arg Ala Lys Thr Gly Gly Thr
 435 440 445
 Val Ser Asp Gln Ala Leu Leu Phe Glu
 450 455

<210> 25

<211> 921

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
h_nh0443k08_A

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 aatttccaag ccaagcctga tgatcttatt ctggcaactt acccaaagtc aggtacaaca 180
 tggatgcatg aaattttaga catgattcta aatgatggtg atgtggagaa atgcaaaaga 240
 gccagactc tagatagaca cgctttcctt gaactgaaat ttcccataa agaaaaacca 300
 gatttggagt tcgttcttga aatgtcctca ccacaactga taaaaacaca tctccttca 360
 catctgattc caccatctat ctggaaagaa aactgcaaga ttgtctatgt ggccagaaat 420

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cccaaggatt gcctggtgtc ctactaccac tttcacagga tggcttcctt tatgcctgat 480
cctcagaact tagaggaatt ttatgagaaa ttcattgtccg gaaaagggtga gttcgggtcc 540
tggtttgacc atgtgaaagg atggtgggct gcaaaagaca tgcaccggat cctctacctc 600
ttctacgagg atattaaaca gaatccaaaa catgagatcc acaagggtgtt ggaattcttg 660
gagaaaaactt ggtcagggtga tgttataaac aagattgtcc accatacctc atttgatgta 720
atgaaggata atcccatggc caaccatact gcggtacctg ctcacatatt caatcactcc 780
atctcaaaat ttatgaggaa aggtgggatg cctggagact ggaagaacca ctttactgtg 840
gctttgaatg agaactttga taagcattat gaaaagaaga tggcagggtc cacactgaac 900
ttctgcctgg agatctgaga g                                     921

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<210> 26

<211> 305

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

h_nh0443k08_A

<400> 26

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Leu Phe Asn Ile Met Glu Val Asp Gly Val Pro Thr Leu Ile Leu Ser
          20           25           30

```

```

Lys Glu Trp Trp Glu Lys Val Cys Asn Phe Gln Ala Lys Pro Asp Asp
          35           40           45

```

```

Leu Ile Leu Ala Thr Tyr Pro Lys Ser Gly Thr Thr Trp Met His Glu
          50           55           60

```

```

Ile Leu Asp Met Ile Leu Asn Asp Gly Asp Val Glu Lys Cys Lys Arg
          65           70           75           80

```

```

Ala Gln Thr Leu Asp Arg His Ala Phe Leu Glu Leu Lys Phe Pro His
          85           90           95

```

```

Lys Glu Lys Pro Asp Leu Glu Phe Val Leu Glu Met Ser Ser Pro Gln
          100          105          110

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```

Leu Ile Lys Thr His Leu Pro Ser His Leu Ile Pro Pro Ser Ile Trp
          115          120          125

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```

Lys Glu Asn Cys Lys Ile Val Tyr Val Ala Arg Asn Pro Lys Asp Cys
          130          135          140

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Leu Val Ser Tyr Tyr His Phe His Arg Met Ala Ser Phe Met Pro Asp
          145          150          155          160

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Pro Gln Asn Leu Glu Glu Phe Tyr Glu Lys Phe Met Ser Gly Lys Gly
          165          170          175

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```

Glu Phe Gly Ser Trp Phe Asp His Val Lys Gly Trp Trp Ala Ala Lys
          180          185          190

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Asp Met His Arg Ile Leu Tyr Leu Phe Tyr Glu Asp Ile Lys Gln Asn
195 200 205

Pro Lys His Glu Ile His Lys Val Leu Glu Phe Leu Glu Lys Thr Trp
210 215 220

Ser Gly Asp Val Ile Asn Lys Ile Val His His Thr Ser Phe Asp Val
225 230 235 240

Met Lys Asp Asn Pro Met Ala Asn His Thr Ala Val Pro Ala His Ile
245 250 255

Phe Asn His Ser Ile Ser Lys Phe Met Arg Lys Gly Gly Met Pro Gly
260 265 270

Asp Trp Lys Asn His Phe Thr Val Ala Leu Asn Glu Asn Phe Asp Lys
275 280 285

His Tyr Glu Lys Lys Met Ala Gly Ser Thr Leu Asn Phe Cys Leu Glu
290 295 300

Ile
305

<210> 27

<211> 893

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
h_nh0778p17_A

<400> 27

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agacagtcac gtatcaacta cagaaacaga ggaacaaggg gtgtttctac agcaagctgt 120
tatttatgaa agagagcctg tagctgagag acacctacat gaaatccaaa aactacagga 180
aagtattaac aatttggcag ataatgttca aaaatttggg cagcaacaga aaagtctggt 240
ggcttcaatg agaaggttta gtctacttaa gagagagtct accattacaa aggagataaa 300
aattcaggca gaatacatca acagaagttt gaatgattta gttaaagaag ttaaaaagtc 360
agaggttgaa aatggtccat cttcagtggt cacaaggata cttaaattctc agcatgctgc 420
aatgttccgc cattttcagc aaatcatggt tatatacaat gacacaatag cagcaaagca 480
agagaagtgc aagacattta ttttacgtca gcttgaagtt gctggaaaag agatgtctga 540
agaagatgta aatgatatgc ttcacatcagg aaaatgggaa gtttttaattg aaagcttact 600
tacagaaatc aatatcacta aagcacaact ttcagagatt gaacagagac acaaggaact 660
tgtaatttg gagaaccaa taaaggattt aagggatctt ttcattcaga tatctctttt 720
agtagaggaa caaggagaga gcatcaacaa tattgaaatg acagtgaata gtacaaaaga 780
gtatgttaac aatactaaag agaaatttgg actagctgta aaatacaaaa aaagaaatcc 840
ttgcagagta ctgtgttggt ggtgctgtcc atgctgtagc tcaaaataaa gaa 893

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<210> 28

<211> 294

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
h_nh0778p17_A

<400> 28

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Arg | Leu | Gln | Glu | Leu | Lys | Gln | Arg | Thr | Lys | Glu | Ile | Glu | 1 | | 5 | | 10 | | 15 |
| Leu | Ser | Arg | Asp | Ser | His | Val | Ser | Thr | Thr | Glu | Thr | Glu | Glu | Gln | Gly | | 20 | | 25 | | 30 | |
| Val | Phe | Leu | Gln | Gln | Ala | Val | Ile | Tyr | Glu | Arg | Glu | Pro | Val | Ala | Glu | | 35 | | 40 | | 45 | |
| Arg | His | Leu | His | Glu | Ile | Gln | Lys | Leu | Gln | Glu | Ser | Ile | Asn | Asn | Leu | 50 | | 55 | | 60 | | |
| Ala | Asp | Asn | Val | Gln | Lys | Phe | Gly | Gln | Gln | Gln | Lys | Ser | Leu | Val | Ala | 65 | | 70 | | 75 | | 80 |
| Ser | Met | Arg | Arg | Phe | Ser | Leu | Leu | Lys | Arg | Glu | Ser | Thr | Ile | Thr | Lys | | 85 | | 90 | | 95 | |
| Glu | Ile | Lys | Ile | Gln | Ala | Glu | Tyr | Ile | Asn | Arg | Ser | Leu | Asn | Asp | Leu | | 100 | | 105 | | 110 | |
| Val | Lys | Glu | Val | Lys | Lys | Ser | Glu | Val | Glu | Asn | Gly | Pro | Ser | Ser | Val | | 115 | | 120 | | 125 | |
| Val | Thr | Arg | Ile | Leu | Lys | Ser | Gln | His | Ala | Ala | Met | Phe | Arg | His | Phe | 130 | | 135 | | 140 | | |
| Gln | Gln | Ile | Met | Phe | Ile | Tyr | Asn | Asp | Thr | Ile | Ala | Ala | Lys | Gln | Glu | 145 | | 150 | | 155 | | 160 |
| Lys | Cys | Lys | Thr | Phe | Ile | Leu | Arg | Gln | Leu | Glu | Val | Ala | Gly | Lys | Glu | | 165 | | 170 | | 175 | |
| Met | Ser | Glu | Glu | Asp | Val | Asn | Asp | Met | Leu | His | Gln | Gly | Lys | Trp | Glu | | 180 | | 185 | | 190 | |
| Val | Phe | Asn | Glu | Ser | Leu | Leu | Thr | Glu | Ile | Asn | Ile | Thr | Lys | Ala | Gln | | 195 | | 200 | | 205 | |
| Leu | Ser | Glu | Ile | Glu | Gln | Arg | His | Lys | Glu | Leu | Val | Asn | Leu | Glu | Asn | 210 | | 215 | | 220 | | |
| Gln | Ile | Lys | Asp | Leu | Arg | Asp | Leu | Phe | Ile | Gln | Ile | Ser | Leu | Leu | Val | 225 | | 230 | | 235 | | 240 |
| Glu | Glu | Gln | Gly | Glu | Ser | Ile | Asn | Asn | Ile | Glu | Met | Thr | Val | Asn | Ser | | 245 | | 250 | | 255 | |
| Thr | Lys | Glu | Tyr | Val | Asn | Asn | Thr | Lys | Glu | Lys | Phe | Gly | Leu | Ala | Val | | 260 | | 265 | | 270 | |
| Lys | Tyr | Lys | Lys | Arg | Asn | Pro | Cys | Arg | Val | Leu | Cys | Cys | Trp | Cys | Cys | 275 | | 280 | | 285 | | |

Pro Cys Cys Ser Ser Lys
290

<210> 29
<211> 892
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
hnh0778p17_A1

<400> 29
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atztatgaaa gagagcctgt agctgagaga cacctacatg aaatccaaaa actacaggaa 180
agtattaaca atttggcaga taatgttcaa aaatttgggc agcaacagaa aagtcctggtg 240
gcttcaatga gaagggttag tctacttaag agagagtcta ccattacaaa ggagataaaa 300
attcaggcag aatacatcaa cagaagtttg aatgatttag ttaaagaagt taaaaagtca 360
gaggttgaaa atggtccatc ttcagtgggc acaaggatac ttaaattctca gcatgctgca 420
atgttccgcc attttcagca aatcatgttt atatacaatg acacaatagc agcaaagcaa 480
gagaagtgca agacatttat tttacgtcag cttgaagttg ctggaaaaga gatgtctgaa 540
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acagaaatca atatcactaa agcacaactt tcagagattg aacagagaca caaggaactt 660
gttaatttgg agaaccaaat aaaggattta agggatcttt tcattcagat atctctttta 720
gtagaggaac aaggagagag catcaacaat attgaaatga cagtgaatag tacaaaagag 780
tatgttaaca atactaaaga gaaatttgga ctagtgtgaa aatacaaaaa aagaaatcct 840
tgcagagtac tgtgtgtgtg gtgctgtcca tgcgtgtagt caaaataaag aa 892

<210> 30
<211> 294
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
hnh0778p17_A1

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Met Lys Asp Arg Leu Gln Glu Leu Lys Gln Arg Thr Lys Glu Ile Glu
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20 25 30
Val Phe Leu Gln Gln Ala Val Ile Tyr Glu Arg Glu Pro Val Ala Glu
35 40 45
Arg His Leu His Glu Ile Gln Lys Leu Gln Glu Ser Ile Asn Asn Leu
50 55 60
Ala Asp Asn Val Gln Lys Phe Gly Gln Gln Gln Lys Ser Leu Val Ala
65 70 75 80

Ser Met Arg Arg Phe Ser Leu Leu Lys Arg Glu Ser Thr Ile Thr Lys
 85 90 95
 Glu Ile Lys Ile Gln Ala Glu Tyr Ile Asn Arg Ser Leu Asn Asp Leu
 100 105 110
 Val Lys Glu Val Lys Lys Ser Glu Val Glu Asn Gly Pro Ser Ser Val
 115 120 125
 Val Thr Arg Ile Leu Lys Ser Gln His Ala Ala Met Phe Arg His Phe
 130 135 140
 Gln Gln Ile Met Phe Ile Tyr Asn Asp Thr Ile Ala Ala Lys Gln Glu
 145 150 155 160
 Lys Cys Lys Thr Phe Ile Leu Arg Gln Leu Glu Val Ala Gly Lys Glu
 165 170 175
 Met Ser Glu Glu Asp Val Asn Asp Met Leu His Gln Gly Lys Trp Glu
 180 185 190
 Val Phe Asn Glu Ser Leu Leu Thr Glu Ile Asn Ile Thr Lys Ala Gln
 195 200 205
 Leu Ser Glu Ile Glu Gln Arg His Lys Glu Leu Val Asn Leu Glu Asn
 210 215 220
 Gln Ile Lys Asp Leu Arg Asp Leu Phe Ile Gln Ile Ser Leu Leu Val
 225 230 235 240
 Glu Glu Gln Gly Glu Ser Ile Asn Asn Ile Glu Met Thr Val Asn Ser
 245 250 255
 Thr Lys Glu Tyr Val Asn Asn Thr Lys Glu Lys Phe Gly Leu Ala Val
 260 265 270
 Lys Tyr Lys Lys Arg Asn Pro Cys Arg Val Leu Cys Cys Trp Cys Cys
 275 280 285
 Pro Cys Cys Ser Ser Lys
 290

<210> 31

<211> 892

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
CG55655_02

<400> 31

aagatgaaag accgacttca agaactaaag cagagaacaa aggaaattga actctctaga 60
 gacagtcatg tatcaactac agaaacagag gaacaagggg tgtttctaca gcaagctggt 120
 atttatgaaa gagagcctgt agctgagaga cacctacatg aaatccaaaa actacaggaa 180
 agtattaaca atttggcaga taatgttcaa aaatttgggc agcaacagaa aagtctggtg 240
 gcttcaatga gaaggtttag tctacttaag agagagtcta ccattacaaa ggagataaaa 300

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attcaggcag aatacatcaa cagaagtttg aatgatttag ttaaagaagt taaaaagtca 360
gagggttgaat atgggtccatc ttcagtgggc acaaggatac ttaaattctca gcatgctgca 420
atgttccgcc atttttcagca aatcatgttt atatacaatg acacaatagc agcaaagcaa 480
gagaagtgca agacatttat ttacgtcag cttgaagttg ctggaaaaga gatgtctgaa 540
gaagatgtaa atgatatgct tcatcaagga aaatgggaag tttttaatga aagcttactt 600
acagaaatca atatcactaa agcacaactt tcagagattg aacagagaca caaggaactt 660
gttaatttgg agaaccacaaat aaaggattta agggatcttt tcattcagat atctctttta 720
gtagaggaac aaggagagag catcaacaat attgaaatga cagtgaatag tacaaaagag 780
tatgttaaca atactaaaga gaaatttgga ctagctgtaa aatacaaaaa aagaaatcct 840
tgcagagtac tgtgttggtg gtgctgtcca tgctgtagct caaaataaag aa 892

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<210> 32

<211> 294

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
CG55655_02

<400> 32

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Met Lys Asp Arg Leu Gln Glu Leu Lys Gln Arg Thr Lys Glu Ile Glu
  1                      5                      10                      15

Leu Ser Arg Asp Ser His Val Ser Thr Thr Glu Thr Glu Glu Gln Gly
                20                      25                      30

Val Phe Leu Gln Gln Ala Val Ile Tyr Glu Arg Glu Pro Val Ala Glu
    35                      40                      45

Arg His Leu His Glu Ile Gln Lys Leu Gln Glu Ser Ile Asn Asn Leu
    50                      55                      60

Ala Asp Asn Val Gln Lys Phe Gly Gln Gln Gln Lys Ser Leu Val Ala
    65                      70                      75                      80

Ser Met Arg Arg Phe Ser Leu Leu Lys Arg Glu Ser Thr Ile Thr Lys
                85                      90                      95

Glu Ile Lys Ile Gln Ala Glu Tyr Ile Asn Arg Ser Leu Asn Asp Leu
    100                      105                      110

Val Lys Glu Val Lys Lys Ser Glu Val Glu Asn Gly Pro Ser Ser Val
    115                      120                      125

Val Thr Arg Ile Leu Lys Ser Gln His Ala Ala Met Phe Arg His Phe
    130                      135                      140

Gln Gln Ile Met Phe Ile Tyr Asn Asp Thr Ile Ala Ala Lys Gln Glu
    145                      150                      155                      160

Lys Cys Lys Thr Phe Ile Leu Arg Gln Leu Glu Val Ala Gly Lys Glu
                165                      170                      175

Met Ser Glu Glu Asp Val Asn Asp Met Leu His Gln Gly Lys Trp Glu
    180                      185                      190

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Val Phe Asn Glu Ser Leu Leu Thr Glu Ile Asn Ile Thr Lys Ala Gln
 195 200 205

Leu Ser Glu Ile Glu Gln Arg His Lys Glu Leu Val Asn Leu Glu Asn
 210 215 220

Gln Ile Lys Asp Leu Arg Asp Leu Phe Ile Gln Ile Ser Leu Leu Val
 225 230 235 240

Glu Glu Gln Gly Glu Ser Ile Asn Asn Ile Glu Met Thr Val Asn Ser
 245 250 255

Thr Lys Glu Tyr Val Asn Asn Thr Lys Glu Lys Phe Gly Leu Ala Val
 260 265 270

Lys Tyr Lys Lys Arg Asn Pro Cys Arg Val Leu Cys Cys Trp Cys Cys
 275 280 285

Pro Cys Cys Ser Ser Lys
 290

<210> 33
 <211> 967
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 GM_11817402_A

<400> 33
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 agtgggtcca gcagatggaa acacagctgc caagtctgcc cctgtcctta gcttctgcag 120
 gaggtgtggg gaactctgcc ttctacaatg tgatgctgca cagagagctg tctgtcatct 180
 tcgaccaatt ccatggcatt caggacactg tgatagggga aggaacgcac tttctcatcc 240
 catgggaaaa gaaaccaatt atttttgact gctgctctcg accacattat gcaccaatca 300
 tcaactgtgag caaagattgt caccatgtca ccatcacact gggcgtcttc tccccgctt 360
 gttgctggcc aggtccttgc atcttccaat tactggagaa gccaatgaag aatgtgctgc 420
 catccatcac tgcggagctc ctcaagctgg gggcggtca ggctgacgct ggagaactga 480
 tcacgcaggg agagctgggc tccagacagg tgagcgagca attaaactgag caagcagcaa 540
 cctttgggtt cctcctggat gctgtgacct tggatctgac cttcgggaag gaatttgcag 600
 aagcagtgga accaaaggag gtggctcagc aggaagaaga gagggccaga tctgtggtgg 660
 caagggctga gcagcagaag acggcggccca tcatctctgc cgagggcgac tccaaggcca 720
 cggagtcat cgccagctca gtggccaccg caggtgacgg cctgatcaag gcccacaagc 780
 tggaaccatg gaggacactg gccctccagc tctcagaact catccacctc atccacctgc 840
 ccgtggggac atctgtgctc ctccagctgc cccagcgag gccgcctga cctgcacctc 900
 ctccagccaa ctggggccaca gcaccaatga cttttactac cgccttcctt ctgtccccc 960
 tccagaa 967

<210> 34
 <211> 271
 <212> PRT
 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
GM_11817402_A

<400> 34

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Gln | Leu | Pro | Ser | Leu | Pro | Leu | Ser | Leu | Ala | Ser | Ala | Gly | 1 | 5 | 10 | 15 |
| Gly | Val | Gly | Asn | Ser | Ala | Phe | Tyr | Asn | Val | Met | Leu | His | Arg | Glu | Leu | 20 | 25 | 30 | |
| Ser | Val | Ile | Phe | Asp | Gln | Phe | His | Gly | Ile | Gln | Asp | Thr | Val | Ile | Gly | 35 | 40 | 45 | |
| Glu | Gly | Thr | His | Phe | Leu | Ile | Pro | Trp | Glu | Lys | Lys | Pro | Ile | Ile | Phe | 50 | 55 | 60 | |
| Asp | Cys | Cys | Ser | Arg | Pro | His | Tyr | Ala | Pro | Ile | Ile | Thr | Val | Ser | Lys | 65 | 70 | 75 | 80 |
| Asp | Cys | His | His | Val | Thr | Ile | Thr | Leu | Gly | Val | Leu | Phe | Pro | Pro | Cys | 85 | 90 | 95 | |
| Cys | Trp | Pro | Gly | Pro | Cys | Ile | Phe | Gln | Leu | Leu | Glu | Lys | Pro | Met | Lys | 100 | 105 | 110 | |
| Asn | Val | Leu | Pro | Ser | Ile | Thr | Ala | Glu | Leu | Leu | Lys | Leu | Gly | Ala | Ala | 115 | 120 | 125 | |
| Gln | Ala | Asp | Ala | Gly | Glu | Leu | Ile | Thr | Gln | Gly | Glu | Leu | Gly | Ser | Arg | 130 | 135 | 140 | |
| Gln | Val | Ser | Glu | Gln | Leu | Thr | Glu | Gln | Ala | Ala | Thr | Phe | Gly | Phe | Leu | 145 | 150 | 155 | 160 |
| Leu | Asp | Ala | Val | Thr | Leu | Asp | Leu | Thr | Phe | Gly | Lys | Glu | Phe | Ala | Glu | 165 | 170 | 175 | |
| Ala | Val | Glu | Pro | Lys | Glu | Val | Ala | Gln | Gln | Glu | Glu | Glu | Arg | Ala | Arg | 180 | 185 | 190 | |
| Ser | Val | Val | Ala | Arg | Ala | Glu | Gln | Gln | Lys | Thr | Ala | Ala | Ile | Ile | Ser | 195 | 200 | 205 | |
| Ala | Glu | Gly | Asp | Ser | Lys | Ala | Thr | Glu | Phe | Ile | Ala | Ser | Ser | Val | Ala | 210 | 215 | 220 | |
| Thr | Ala | Gly | Asp | Gly | Leu | Ile | Lys | Ala | His | Lys | Leu | Glu | Pro | Trp | Arg | 225 | 230 | 235 | 240 |
| Thr | Leu | Ala | Leu | Gln | Leu | Ser | Glu | Leu | Ile | His | Leu | Ile | His | Leu | Pro | 245 | 250 | 255 | |
| Val | Gly | Thr | Ser | Val | Leu | Leu | Gln | Leu | Pro | Gln | Arg | Arg | Pro | Pro | 260 | 265 | 270 | | |

<210> 35
 <211> 464
 <212> PRT
 <213> Rattus norvegicus

<400> 35
 Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
 1 5 10 15
 Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
 20 25 30
 Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
 35 40 45
 Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
 50 55 60
 Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
 65 70 75 80
 Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
 85 90 95
 Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
 100 105 110
 Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
 115 120 125
 Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
 130 135 140
 His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
 145 150 155 160
 Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
 165 170 175
 Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
 180 185 190
 Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
 195 200 205
 Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
 210 215 220
 His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
 225 230 235 240
 Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
 245 250 255
 Asn Phe Val Leu Arg Arg His Ile Phe Phe Phe Val Leu Gln Thr Tyr
 260 265 270

Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285
 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300
 Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 36

<211> 464

<212> PRT

<213> Rattus norvegicus

<400> 36

Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
 1 5 10 15
 Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
 20 25 30
 Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
 35 40 45
 Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
 50 55 60
 Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
 65 70 75 80

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Gly | Ile | Asp | Val | Gln | Val | Glu | Ser | Ile | Asp | Ser | Ile | Ser | Glu | 85 | 90 | 95 |
| Val | Asn | Met | Asp | Phe | Thr | Met | Thr | Phe | Tyr | Leu | Arg | His | Tyr | Trp | Lys | 100 | 105 | 110 |
| Asp | Glu | Arg | Leu | Ser | Phe | Pro | Ser | Thr | Thr | Asn | Lys | Ser | Met | Thr | Phe | 115 | 120 | 125 |
| Asp | Arg | Arg | Leu | Ile | Gln | Lys | Ile | Trp | Val | Pro | Asp | Ile | Phe | Phe | Val | 130 | 135 | 140 |
| His | Ser | Lys | Arg | Ser | Phe | Ile | His | Asp | Thr | Thr | Val | Glu | Asn | Ile | Met | 145 | 150 | 155 |
| Leu | Arg | Val | His | Pro | Asp | Gly | Asn | Val | Leu | Phe | Ser | Leu | Arg | Ile | Thr | 165 | 170 | 175 |
| Val | Ser | Ala | Met | Cys | Phe | Met | Asp | Phe | Ser | Arg | Phe | Pro | Leu | Asp | Thr | 180 | 185 | 190 |
| Gln | Asn | Cys | Ser | Leu | Glu | Leu | Glu | Ser | Tyr | Ala | Tyr | Asn | Glu | Glu | Asp | 195 | 200 | 205 |
| Leu | Met | Leu | Tyr | Trp | Lys | His | Gly | Asn | Lys | Ser | Leu | Asn | Thr | Glu | Glu | 210 | 215 | 220 |
| His | Ile | Ser | Leu | Ser | Gln | Phe | Phe | Ile | Glu | Glu | Phe | Ser | Ala | Ser | Ser | 225 | 230 | 235 |
| Gly | Leu | Ala | Phe | Tyr | Ser | Ser | Thr | Gly | Trp | Tyr | Tyr | Arg | Leu | Phe | Ile | 245 | 250 | 255 |
| Asn | Phe | Val | Leu | Arg | Arg | His | Ile | Phe | Phe | Phe | Val | Leu | Gln | Thr | Tyr | 260 | 265 | 270 |
| Phe | Pro | Ala | Met | Leu | Met | Val | Met | Leu | Ser | Trp | Val | Ser | Phe | Trp | Ile | 275 | 280 | 285 |
| Asp | Arg | Arg | Ala | Val | Pro | Ala | Arg | Val | Ser | Leu | Gly | Ile | Thr | Thr | Val | 290 | 295 | 300 |
| Leu | Thr | Met | Ser | Thr | Ile | Val | Thr | Gly | Val | Ser | Ala | Ser | Met | Pro | Gln | 305 | 310 | 315 |
| Val | Ser | Tyr | Val | Lys | Ala | Val | Asp | Val | Tyr | Met | Trp | Val | Ser | Ser | Leu | 325 | 330 | 335 |
| Phe | Val | Phe | Leu | Ser | Val | Ile | Glu | Tyr | Ala | Ala | Val | Asn | Tyr | Leu | Thr | 340 | 345 | 350 |
| Thr | Val | Glu | Glu | Trp | Lys | Gln | Leu | Asn | Arg | Arg | Gly | Lys | Ile | Ser | Gly | 355 | 360 | 365 |
| Met | Tyr | Asn | Ile | Asp | Ala | Val | Gln | Ala | Met | Ala | Phe | Asp | Gly | Cys | Tyr | 370 | 375 | 380 |

His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
385 390 395 400

Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
405 410 415

Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
420 425 430

Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
435 440 445

Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
450 455 460

<210> 37

<211> 464

<212> PRT

<213> Rattus norvegicus

<400> 37

Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
1 5 10 15

Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
20 25 30

Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
35 40 45

Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
50 55 60

Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
65 70 75 80

Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
85 90 95

Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
100 105 110

Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
115 120 125

Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
130 135 140

His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
145 150 155 160

Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
165 170 175

Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
180 185 190

Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
 195 200 205
 Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
 210 215 220
 His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
 225 230 235 240
 Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
 245 250 255
 Asn Phe Val Leu Arg Arg His Ile Phe Phe Phe Val Leu Gln Thr Tyr
 260 265 270
 Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285
 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300
 Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 38

<211> 464

<212> PRT

<213> Rattus norvegicus

<400> 38

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Ala | Phe | Trp | Leu | Ala | Phe | Phe | Thr | Tyr | Thr | Trp | Ile | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Met | Leu | Asp | Ala | Ser | Ala | Val | Lys | Glu | Pro | His | Gln | Gln | Cys | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Ser | Pro | Lys | Gln | Thr | Arg | Ile | Arg | Glu | Thr | Arg | Met | Arg | Lys | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Leu | Thr | Lys | Val | Trp | Pro | Leu | Lys | Arg | Glu | Gln | Leu | Leu | His | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Asp | His | Asp | Phe | Ser | Thr | Arg | Pro | Gly | Phe | Gly | Gly | Ser | Pro | Val |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Val | Gly | Ile | Asp | Val | Gln | Val | Glu | Ser | Ile | Asp | Ser | Ile | Ser | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Asn | Met | Asp | Phe | Thr | Met | Thr | Phe | Tyr | Leu | Arg | His | Tyr | Trp | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asp | Glu | Arg | Leu | Ser | Phe | Pro | Ser | Thr | Thr | Asn | Lys | Ser | Met | Thr | Phe |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Asp | Arg | Arg | Leu | Ile | Gln | Lys | Ile | Trp | Val | Pro | Asp | Ile | Phe | Phe | Val |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| His | Ser | Lys | Arg | Ser | Phe | Ile | His | Asp | Thr | Thr | Val | Glu | Asn | Ile | Met |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Arg | Val | His | Pro | Asp | Gly | Asn | Val | Leu | Phe | Ser | Leu | Arg | Ile | Thr |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Val | Ser | Ala | Met | Cys | Phe | Met | Asp | Phe | Ser | Arg | Phe | Pro | Leu | Asp | Thr |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gln | Asn | Cys | Ser | Leu | Glu | Leu | Glu | Ser | Tyr | Ala | Tyr | Asn | Glu | Glu | Asp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Met | Leu | Tyr | Trp | Lys | His | Gly | Asn | Lys | Ser | Leu | Asn | Thr | Glu | Glu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| His | Ile | Ser | Leu | Ser | Gln | Phe | Phe | Ile | Glu | Glu | Phe | Ser | Ala | Ser | Ser |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 |
| Gly | Leu | Ala | Phe | Tyr | Ser | Ser | Thr | Gly | Trp | Tyr | Tyr | Arg | Leu | Phe | Ile |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Asn | Phe | Val | Leu | Arg | Arg | His | Ile | Phe | Phe | Phe | Val | Leu | Gln | Thr | Tyr |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Phe | Pro | Ala | Met | Leu | Met | Val | Met | Leu | Ser | Trp | Val | Ser | Phe | Trp | Ile |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Asp | Arg | Arg | Ala | Val | Pro | Ala | Arg | Val | Ser | Leu | Gly | Ile | Thr | Thr | Val |
| | 290 | | | | | 295 | | | | | 300 | | | | |

Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 39

<211> 392

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (111)

<223> Any amino acid

<400> 39

Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
 1 5 10 15
 Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
 20 25 30
 Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
 35 40 45
 Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
 50 55 60
 Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65 70 75 80

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Trp | Asn | Met | Ser | Glu | Cys | Gly | Gly | Leu | Cys | Gln | Pro | Thr | Glu | Tyr | 85 | 90 | 95 |
| Ser | Ala | Asp | Gly | Phe | Ala | Pro | Cys | Gln | Leu | Cys | Ala | Leu | Gly | Xaa | Phe | 100 | 105 | 110 |
| Gln | Pro | Glu | Ala | Gly | Arg | Thr | Ser | Cys | Phe | Pro | Cys | Gly | Gly | Gly | Leu | 115 | 120 | 125 |
| Ala | Thr | Lys | His | Gln | Gly | Ala | Thr | Ser | Phe | Gln | Asp | Cys | Glu | Thr | Arg | 130 | 135 | 140 |
| Val | Gln | Cys | Ser | Pro | Gly | His | Phe | Tyr | Asn | Thr | Thr | Thr | His | Arg | Cys | 145 | 150 | 155 |
| Ile | Arg | Cys | Pro | Val | Gly | Thr | Tyr | Gln | Pro | Glu | Phe | Gly | Lys | Asn | Asn | 165 | 170 | 175 |
| Cys | Val | Ser | Cys | Pro | Gly | Asn | Thr | Thr | Thr | Asp | Phe | Asp | Gly | Ser | Thr | 180 | 185 | 190 |
| Asn | Ile | Thr | Gln | Cys | Lys | Asn | Arg | Arg | Cys | Gly | Gly | Glu | Leu | Gly | Asp | 195 | 200 | 205 |
| Phe | Thr | Gly | Tyr | Ile | Glu | Ser | Pro | Asn | Tyr | Pro | Gly | Asn | Tyr | Pro | Ala | 210 | 215 | 220 |
| Asn | Thr | Glu | Cys | Thr | Trp | Thr | Ile | Asn | Pro | Pro | Pro | Lys | Arg | Arg | Ile | 225 | 230 | 235 |
| Leu | Ile | Val | Val | Pro | Glu | Ile | Phe | Leu | Pro | Ile | Glu | Asp | Asp | Cys | Gly | 245 | 250 | 255 |
| Asp | Tyr | Leu | Val | Met | Arg | Lys | Thr | Ser | Ser | Ser | Asn | Ser | Val | Thr | Thr | 260 | 265 | 270 |
| Tyr | Glu | Thr | Cys | Gln | Thr | Tyr | Glu | Arg | Pro | Ile | Ala | Phe | Thr | Ser | Arg | 275 | 280 | 285 |
| Ser | Lys | Lys | Leu | Trp | Ile | Gln | Phe | Lys | Ser | Asn | Glu | Gly | Asn | Ser | Ala | 290 | 295 | 300 |
| Arg | Gly | Phe | Gln | Val | Pro | Tyr | Val | Thr | Tyr | Asp | Glu | Asp | Tyr | Gln | Glu | 305 | 310 | 315 |
| Leu | Ile | Glu | Asp | Ile | Val | Arg | Asp | Gly | Arg | Leu | Tyr | Ala | Ser | Glu | Asn | 325 | 330 | 335 |
| His | Gln | Glu | Ile | Leu | Lys | Asp | Lys | Lys | Leu | Ile | Lys | Ala | Leu | Phe | Asp | 340 | 345 | 350 |
| Val | Leu | Ala | His | Pro | Gln | Asn | Tyr | Phe | Lys | Tyr | Thr | Ala | Gln | Glu | Ser | 355 | 360 | 365 |
| Arg | Glu | Met | Phe | Pro | Arg | Ser | Phe | Ile | Arg | Leu | Leu | Arg | Ser | Lys | Val | 370 | 375 | 380 |

Ser Arg Phe Leu Arg Pro Tyr Lys
385 390

<210> 40

<211> 283

<212> PRT

<213> Rattus norvegicus

<400> 40

Glu Val Asn Gly Ile Leu Met Ser Lys Leu Met Ser Asp Asn Trp Asp
1 5 10 15

Lys Ile Trp Asn Phe Gln Ala Lys Pro Asp Asp Leu Leu Ile Ala Thr
20 25 30

Tyr Ala Lys Ala Gly Thr Thr Trp Thr Gln Glu Ile Val Asp Met Ile
35 40 45

Gln Asn Asp Gly Asp Val Gln Lys Cys Gln Arg Ala Asn Thr Tyr Asp
50 55 60

Arg His Pro Phe Ile Glu Trp Thr Leu Pro Ser Pro Leu Asn Ser Gly
65 70 75 80

Leu Asp Leu Ala Asn Lys Met Pro Ser Pro Arg Thr Leu Lys Thr His
85 90 95

Leu Pro Val His Met Leu Pro Pro Ser Phe Trp Lys Glu Asn Ser Lys
100 105 110

Ile Ile Tyr Val Ala Arg Asn Ala Lys Asp Cys Leu Val Ser Tyr Tyr
115 120 125

Tyr Phe Ser Arg Met Asn Lys Met Leu Pro Asp Pro Gly Thr Leu Gly
130 135 140

Glu Tyr Ile Glu Gln Phe Lys Ala Gly Lys Val Leu Trp Gly Ser Trp
145 150 155 160

Tyr Asp His Val Lys Gly Trp Trp Asp Val Lys Asp Gln His Arg Ile
165 170 175

Leu Tyr Leu Phe Tyr Glu Asp Met Lys Glu Asp Pro Lys Arg Glu Ile
180 185 190

Lys Lys Ile Ala Lys Phe Leu Glu Lys Asp Ile Ser Glu Glu Val Leu
195 200 205

Asn Lys Ile Ile Tyr His Thr Ser Phe Asp Val Met Lys Glu Asn Pro
210 215 220

Met Ala Asn Tyr Thr Thr Leu Pro Ser Ser Ile Met Asp His Ser Ile
225 230 235 240

Ser Pro Phe Met Arg Lys Gly Met Pro Gly Asp Trp Lys Asn Tyr Phe
245 250 255

Thr Val Ala Gln Ser Glu Asp Phe Asp Glu Asp Tyr Arg Arg Lys Met
 260 265 270

Ala Gly Ser Asn Ile Thr Phe Arg Thr Glu Ile
 275 280

<210> 41

<211> 285

<212> PRT

<213> Homo sapiens

<400> 41

Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15

Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30

Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45

Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
 50 55 60

Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80

Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
 85 90 95

Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110

Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
 115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140

Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160

Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190

Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205

Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
 210 215 220

His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240

Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
245 250 255

Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
260 265 270

Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys
275 280 285

<210> 42

<211> 285

<212> PRT

<213> Homo sapiens

<400> 42

Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
1 5 10 15

Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
20 25 30

Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
35 40 45

Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
50 55 60

Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
65 70 75 80

Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
85 90 95

Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
100 105 110

Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
130 135 140

Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
145 150 155 160

Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
180 185 190

Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
195 200 205

Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
210 215 220

His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240

Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
 245 250 255

Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
 260 265 270

Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys
 275 280 285

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 43

ttggaagaga tggtcctggc ttcc

24

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 44

ttcataggat tctcagctgt gtgagt

27

<210> 45

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 45

ttggaagaga tggtcctggc ttcc

24

<210> 46

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 46
ttcataggat tctcagctgt gtgagtg 27

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
gtgtgttcct ctcgactgtg ga 22

<210> 48
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
gacccttgga ccctacttca aa 22

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 49
ccccgatcca gaatggcttc atga 24

<210> 50
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 50
tgtgccgagg gcaacg 16

<210> 51
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe

 <400> 51
 tagctgccca tcatgttgac acagctct 28

 <210> 52
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe

 <400> 52
 agaagccttc ccggcagt 18

 <210> 53
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe

 <400> 53
 cttgtgggcc agctcataat c 21

 <210> 54
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe

 <400> 54
 accgcttcct gctgcgcctg 20

 <210> 55
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe

 <400> 55
 gatgctcaga aagtccatca acc 23

 <210> 56
 <211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 56

cttatgagac ctgccagacc ta

22

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 57

cttcactgcc cgttccagga agct

24

<210> 58

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 58

ctcgcttgtc ttgaagttga tc

22